

Query Match 98.6%; Score 640; DB 2; Length 495;
 Best Local Similarity 98.3%; Pred. No. 1.5e-58;
 Matches 117; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 PLATQGRKPSKRLKARCSRKALHVNFKMGMDMIAPLEYEAHFCEGLCEPRLSHLE 60
 DB 377 PLATQGRKPSKRLKARCSRKALHVNFKMGMDMIAPLEYEAHFCEGLCEPRLSHLE 436

QY 61 PTHNAVITQTLNMSMDPESTPTACVPTRLSPISILFIDSANNVYKQYEDMVVSCGCR 119
 DB 437 PTHNAVITQTLNMSMDPESTPTACVPTRLSPISILFIDSANNVYKQYEDMVVSCGCR 495

RESULT 3
 A55452
 cartilage-derived morphogenetic protein 1 precursor - human
 C:Species: Homo sapiens (man)
 C:Date: 10-Feb-1995 #sequence_revision 10-Feb-1995 #text_change 17-Mar-2000
 C:Accession: A55452
 R:Chang, S.C.; Hoang, B.; Thomas, J.T.; Vukicevic, S.; Luyten, F.P.; Ryba, N.J.P.; Kozak J. Biol. Chem. 269, 28227-28234, 1994
 A:Title: Cartilage-derived morphogenetic proteins. New members of the transforming growth A:Reference number: A55452; MUID:95050604; PMID:7961761
 A:Accession: A55452
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-501 <CHA>
 A:Cross-references: GB:U13660; NID:9600731; PID:9600732
 C:Genetics:
 A:Gene: GDB:CDMP1
 A:Cross-references: GDB:438940
 C:Superfamily: inhibin

Query Match 98.5%; Score 639; DB 2; Length 501;
 Best Local Similarity 98.3%; Pred. No. 1.9e-58;
 Matches 117; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 PLATQGRKPSKRLKARCSRKALHVNFKMGMDMIAPLEYEAHFCEGLCEPRLSHLE 60
 DB 383 PLATQGRKPSKRLKARCSRKALHVNFKMGMDMIAPLEYEAHFCEGLCEPRLSHLE 442

QY 61 PTHNAVITQTLNMSMDPESTPTACVPTRLSPISILFIDSANNVYKQYEDMVVSCGCR 119
 DB 443 PTHNAVITQTLNMSMDPESTPTACVPTRLSPISILFIDSANNVYKQYEDMVVSCGCR 501

RESULT 4
 S43295
 bone morphogenetic protein homolog GDF6 precursor - mouse (fragment)
 N:Alternate names: growth and differentiation factor 6
 C:Species: Mus musculus (house mouse)
 C:Date: 20-Oct-1994 #sequence_revision 07-Feb-1997 #text_change 26-May-2000
 C:Accession: S43295
 R:Storm, E.E.; Huynh, T.V.; Copeland, N.G.; Jenkins, N.A.; Kingsley, D.M.; Lee, S.J. Nature 368, 639-643, 1994
 A:Title: Limb alterations in brachypodism mice due to mutations in a new member of the T A:Reference number: S43294; MUID:94195427; PMID:8145850
 A:Accession: S43295
 A:Molecule type: DNA
 A:Residues: 1-125 <STO>
 A:Cross-references: EMBL:U08338; NID:9488463; PIDN:AAA18779.1; PID:9488464
 C:Genetics:
 A:Gene: Gdf6
 C:Superfamily: inhibin
 P:1-5/Domain: polybasic protease recognition site #status predicted <PPR>
 P:6-125/Product: bone morphogenetic protein homolog GDF6 (fragment) #status predicted <M

Query Match 83.7%; Score 543; DB 2; Length 125;
 Best Local Similarity 80.3%; Pred. No. 3.7e-49;
 Matches 94; Conservative 13; Mismatches 10; Indels 0; Gaps 0;

QY 3 ATROGKRPSKRLKARCSRKALHVNFKMGMDMIAPLEYEAHFCEGLCEPRLSHLEPT 62

DB 9 ASRGRKHGKRSRLKARCSRKALHVNFKMGMDMIAPLEYEAHFCEGLCEPRLSHLEPT 68
 QY 63 NHAVITQTLNMSMDPESTPTACVPTRLSPISILFIDSANNVYKQYEDMVVSCGCR 119
 DB 69 NHAVITQTLNMSMDPESTPTACVPTRLSPISILFIDSANNVYKQYEDMVVSCGCR 125

RESULT 5
 B55452
 cartilage-derived morphogenetic protein 2 precursor - bovine (fragment)
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 10-Feb-1995 #sequence_revision 10-Feb-1995 #text_change 26-May-2000
 C:Accession: B55452
 R:Chang, S.C.; Hoang, B.; Thomas, J.T.; Vukicevic, S.; Luyten, F.P.; Ryba, N.J.P.; Kozak J. Biol. Chem. 269, 28227-28234, 1994
 A:Title: Cartilage-derived morphogenetic proteins. New members of the transforming growth A:Reference number: A55452; MUID:95050604; PMID:7961761
 A:Accession: B55452
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-436 <CHA>
 A:Cross-references: GB:U13661; NID:9632489; PIDN:AAA61416.1; PID:9632490
 C:Superfamily: inhibin

Query Match 81.4%; Score 528; DB 2; Length 436;
 Best Local Similarity 76.9%; Pred. No. 5.4e-47;
 Matches 90; Conservative 16; Mismatches 11; Indels 0; Gaps 0;

QY 3 ATROGKRPSKRLKARCSRKALHVNFKMGMDMIAPLEYEAHFCEGLCEPRLSHLEPT 62
 DB 320 ASRGRKHGKRSRLKARCSRKALHVNFKMGMDMIAPLEYEAHFCEGLCEPRLSHLEPT 379

QY 63 NHAVITQTLNMSMDPESTPTACVPTRLSPISILFIDSANNVYKQYEDMVVSCGCR 119
 DB 380 NHAVITQTLNMSMDPESTPTACVPTRLSPISILFIDSANNVYKQYEDMVVSCGCR 436

RESULT 6
 S43296
 bone morphogenetic protein-related protein (GDF7) - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 20-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 19-May-2000
 C:Accession: S43296
 R:Storm, E.E.; Huynh, T.V.; Copeland, N.G.; Jenkins, N.A.; Kingsley, D.M.; Lee, S.J. Nature 368, 639-643, 1994
 A:Title: Limb alterations in brachypodism mice due to mutations in a new member of the A:Reference number: S43294; MUID:94195427; PMID:8145850
 A:Accession: S43296
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-151 <STO>
 A:Cross-references: GB:U08339; NID:9488465; PIDN:AAA18780.1; PID:9488466
 C:Superfamily: inhibin

Query Match 76.0%; Score 493; DB 2; Length 151;
 Best Local Similarity 73.5%; Pred. No. 7.1e-44;
 Matches 83; Conservative 20; Mismatches 10; Indels 0; Gaps 0;

QY 7 GKRPSKRLKARCSRKALHVNFKMGMDMIAPLEYEAHFCEGLCEPRLSHLEPTNAH 66
 DB 39 GRGRRSRCSKRSKSLHVDYFRELGMWDMIAPLEYEAHFCEGLCEPRLSHLEPTNAH 98

QY 67 IOTLMSMDPESTPTACVPTRLSPISILFIDSANNVYKQYEDMVVSCGCR 119
 DB 99 IOTLMSMDPESTPTACVPTRLSPISILFIDSANNVYKQYEDMVVSCGCR 151

RESULT 7
 S52408
 SPDVA1 protein - sea urchin (Strongylocentrotus purpuratus)
 C:Species: Strongylocentrotus purpuratus (purple urchin)
 C:Date: 08-May-1995 #sequence_revision 21-Jul-1995 #text_change 20-Sep-1999

C:Accession: S52408
R:Ponce, M.R.; Micol, J.L.; Davidson, E.H.
submitted to the EMBL Data Library, February 1995
A:Description: SpbVRI, a member of the transforming growth factor-beta superfamily expressed in the
A:Reference number: S52408
A:Accession: S52408
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-461 <PON>
A:Cross-references: EMBL:Z48313; NID:G673496; PTD:G673497
C:Superfamily: inhibin

| | | | | |
|-----------------------|------------------|--------------------|------------|-------------|
| Query Match | 54.5%; | Score 353.5; | DB 2; | Length 461; |
| Best Local Similarity | 48.1%; | Pred. No. 7.3e-29; | | |
| Matches 65; | Conservative 19; | Mismatches 32; | Indels 19; | Gaps 2; |

```

2Y      3  ATRG---GKRSK-----NLKARCSRKLHVFNDMGWDMTIAPLEYE 43
      ||||  ||||  ||||  ||||  ||||  ||||  ||||  ||||  ||||  ||||
Dib    326  ATRRKGKGRPKPKPTDNDIASDSSASSINSQCKRKILFVNFEEDLDQEWIIAPIGYV 389

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QY 44 AFHCEGLCEPLRSHLEPTNHAIVQLMNSDPSSEPTACTPTRLSPISLFI DSANV 103
||::|:||| ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 386 AFYCGECAPPLNGHANATNHAIVOTLVHNHSPSHVEQPCCAPTSLPI TVAYDDSRNV 445

| | | | |
|----|-----|-----------------|-----|
| QY | 104 | VYKQYEDMWVESGCG | 118 |
| | | : : : : | |
| Db | 446 | VLKKYKNMVRACGC | 460 |

RESULT 8
S37073

C:Species: Rattus norvegicus (Norway rat)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 16-Jul-1999
C:Accession: S37073
R:Feng, J.-Q.; Chen, D.; Feng, M.; Harris, M.A.; Mundy, G.R.; Harris, S.E.
submitted to the EMBL Data Library, September 1993
A:Description: cDNA sequence of fetal rat calvarial osteoblast bone morphogenetic protein
A:Reference number: S37073
A:Accession: S37073
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-393 <FEN>
A:Cross-references: EMBL:Z25868; NID:G397950; FIDN:CAA81086.1; FID:G397951
A:Superfamily: immbin

| | | | | |
|-----------------------|--------|--------------------|--------|----------------|
| Query Match | 53.5%; | Score 347; | DB 2; | Length 393; |
| Best Local Similarity | 54.3%; | Pred. No. 2.9e-28; | | |
| Matches | 63; | Conservative | 17; | Mismatches 34; |
| | | | Indels | 2; |
| | | | Gaps | 2; |

QY 5 RGGK-RPSKKLKARCSRKAHVNFKMGMDWIAPLEIYAAPHCEGTCFEPDRSHLETPTN 63
| | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | :
Db 279 RQAKHKQRKLKSSCKRHPLYVDFSDVGNDWIVAPPGYNAFYCHSGSPFPPLADHLNSTN 338

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Qy      64 HAVIQTIMNSKDESTPTACVPRRLSPILFITSANNVYKQYEDMVVESGCCR 119
        ||::|||:||:| | | | | | | | | | | | | | | | | | | |
Db     339 HAIVQTIVNSVN-SKIIPKACCVPRRLSATMLTYLDENEKVVLKNYQDMVVEGGCCR 393
```

RESULT 9
S45355

Done morphogenetic protein-2 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 10-Dec-1994 #sequence_revision 17-Nov-1995 #text_change 03-May-1996
C:Accession: S45355
R:Feng, J.Q.; Harris, M.A.; Ghosh-Choudhury, N.; Feng, M.; Murdy, G.R.; Harris, S.E.
Biochem. Biophys. Acta 1218, 221-224, 1994
A:Title: Structure and sequence of mouse bone morphogenetic protein-2 gene (BMP-2): comp
A:Reference number: S45355; MUID:94289485; PMID:8018727
A:Accession: S45355
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-394 <FEN>

C;Superfamily: inhibin

| Query Match | Score | DB 2; | Length |
|-------------|-------|-------|--------|
| 53.5%; | 347; | | 394; |

Matches 63; Conservative 17; Mismatches 34; Indels 2; Gaps 2;

[illegible]

D6
QY 64 HAVIQTLNMSNDPESTPPTACVTRLSPILFLDSANNVVKQYEMWVESGCR 119
||::||::|||::|||::|||::|||
Db 340 HAIVQLTVNSVN-SKIPKACCPTELTAISMLYDENEKVYLKNYQDMWVEGGCR 394

RESULT 10

bone morphogenetic protein 2 precursor - human
N/Alternate names: bone morphogenetic protein 2a; rhBMP2
C/Species: Homo sapiens (man)
C/Date: 16-Sep-1992 #sequence__revision 03-Aug-1995 #text__change 18-Jun-1999
C/Accession: B37278; PC2178
R/Money: J.M.; Rosen, V.; Celeste, A.J.; Mltsock, L.M.; Whitters, M.J.; Kitz, R.W.; He
S/Title: Novel regulators of bone formation: molecular clones and activities.
R/Reference number: A37278; MUID:69072730; PMID:3201241

A;Residues: 1-396 <MO2>

A; Cross-references: GB:M22489; NID:gl179501; PIDD:AAA51834.1; PID:gl179502
J; Ishida, N.; Tsujimoto, M.; Kanaya, T.; Shimamura, A.; Tsurutaka, N.; Kodama, S.; Katay
J. Biochem. 115, 279-285, 1994
A; Title: Expression and characterization of human bone morphogenetic protein-2 in silkw
J; Reference number: PC2176; MUID:94266754; PMID:8206877

A;Molecule type: protein
A;Residues: 290-295, 'X',

A; Experimental source: cell line BOMO-15ALLC R; Rathore, S.; Hammerstone, K.M.; Dansereau, S.; Porter, T.J. Protein Sci. 4(Suppl.2): 443S, 1995

A; Reference number: A56729

A:Note: determination of amino ends of mature forms; dimers with long form chains have C:Comment: This hormone is capable of inducing bone formation at ectopic morphological C:Genetics:

```
A:Cross references: GDB:125204; OMIM:112261
A:Map position: 20p12-20p12
```

C;Complex: homodimer, disulfide linked
C;Superfamily: inhibin

F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-265/Domain: propeptide #status predicted <PRO>

E:135,163,164,200/Binding site: carboxylate (Asn) (covalent) #status predicted
E:283-396/Product: bone morphogenetic protein 2 #status predicted <MAN>
E:166-350/Product: bone morphogenetic protein 2, long form #status predicted
E:166-350/Product: bone morphogenetic protein 2, long form #status predicted

F7283/Modified site: pyrrolicone carboxylic acid (Gln) (in mature form) #status experim
F7338/Binding site: carboxylate (Asn) (covalent) #status experimental

Query Match 53.5%; Score 347; DB 1; Length 396;

| | | | | | | | | | |
|---------|-----|--------------|-----|------------|-----|--------|----|------|----|
| Matches | 63; | Conservative | 17; | Mismatches | 34; | Indels | 2; | Gaps | 2; |
|---------|-----|--------------|-----|------------|-----|--------|----|------|----|

Qy 5 RQGK-RPSKULKARCSRKAALHYNFKMGWDWIAPLEAEAFHEGGLCEPPLRSHTEPTN 63
Db 282 RQAKHKQRKLKSSCKRHPLYDFSDVGVNDWIVAPPGYHAFAFYHGEGCEPPLADHLNSTN 34

Qy 64 HAVIQILMSNDPESTPTACTVTRLSPISILEIDSANVVYKQIEDMVESCGCR 119
:::|::| | | | | | | | | | | | | | | |
Db 342 HAIVQTLVNSVA-SKITPRACCPVELSALMLYIDENEKVTLKNYQDMVEEGCCR 390

RESULT 11

JH0689

bone morphogenetic protein 4 precursor - African clawed frog

C:Species: Xenopus laevis (African clawed frog)

C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Jul-1999

C:Accession: JH0689

R:Nishimatsu, S.; Suzuki, A.; Shoda, A.; Murakami, K.; Ueno, N.

Biochem. Biophys. Res. Commun. 186, 1487-1495, 1992

A:Title: Genes for bone morphogenetic proteins are differentially transcribed in early a

A:Reference number: JH0687; MUID:92378616; PMID:1510675

A:Accession: JH0689

A:Molecule type: mRNA

A:Residues: 1-401 <NIS>

A:Cross-references: GB:X63426; NID:964587; PIDN:CA45020.1; PID:964588

A:Experimental source: oocyte

C:Superfamily: inhibin

C:Keywords: glycoprotein

P:288-401/Product: bone morphogenetic protein 4 #status predicted <MAT>

F:141,204,238,343/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match

Best Local Similarity 53.5%; Score 347; DB 2; Length 401;

Matches 63; Conservative 21; Mismatches 31; Indels 6; Gaps 2;

QY

4 TRGGRPSKRLKAR-----CSRKALHVNFKMGMDWIIAPLEYAFHCEGLCEFPRLRSH 58

DB 282 TRRSRSPKQOPRRKKNKCRHSLYVDFSDVGMNDWIVAPPGYQAFYCHGDCPEPLADH 341

QY

59 LEPTNHAIVQTLNMSMDPESTPTACVPTRLSPISILFIDSANNVYQYEDMYESGCG 118

DB 342 LNSTNHAIVQTLVNSVN-SSIPKACCVPTLSAISMLYDEYDKVVLKXNYQEMVVEGCGC 400

QY

119 R 119

DB 401 R 401

QY

DB

QY

DB

QY

DB

QY

DB

QY

DB

QY

DB

QY

DB

QY

DB

QY

DB

QY

DB

QY

DB

QY

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QY

DB

QY

DB

QY

DB

QY

DB

QY

DB

QY

DB

QY

DB

QY

DB

QY

DB

RESULT 13

I50608

bone morphogenetic protein 4 - chicken

C:Species: Gallus gallus (chicken)

C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 16-Jul-1999

C:Accession: I50608

R:Francis, P.H.; Richardson, M.K.; Brickell, P.M.; Tickle, C.

Development 120, 209-218, 1994

A:Title: Bone morphogenetic proteins and a signalling pathway that controls patterning :

A:Reference number: I50607; MUID:94163974; PMID:8119128

A:Accession: I50608

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-405 <FPA>

A:Cross-references: EMBL:X75915; NID:9472929; PIDN:CA45314.1; PID:9472930

C:Genetics: BMP-4

C:Superfamily: inhibin

Query Match

Best Local Similarity 53.3%; Score 346; DB 2; Length 405;

Matches 63; Conservative 21; Mismatches 31; Indels 6; Gaps 2;

QY

4 TRGGRP-----SKRLARCSRKALHVNFKMGMDWIIAPLEYAFHCEGLCEFPRLRSH 58

DB 286 TRRARSPKHHGSRKKNKCRHSLYVDFSDVGMNDWIVAPPGYQAFYCHGDCPEPLADH 345

QY

59 LEPTNHAIVQTLNMSMDPESTPTACVPTRLSPISILFIDSANNVYQYEDMYESGCG 118

DB 346 LNSTNHAIVQTLVNSVN-SSIPKACCVPTLSAISMLYDEYDKVVLKXNYQEMVVEGCGC 404

QY

119 R 119

DB 405 R 405

QY

DB

QY

DB

QY

DB

QY

DB

QY

DB

QY

DB

QY

DB

QY

DB

QY

DB

QY

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QY

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QY

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QY

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QY

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QY

DB

QY

DB

QY

DB

QY

DB

QY

DB

QY

DB

QY

DB

RESULT 14

A26158

decapentaplegic protein precursor - fruit fly (Drosophila melanogaster)

C:Species: Drosophila melanogaster

C:Date: 24-Jun-1987 #sequence_revision 24-Jun-1987 #text_change 16-Apr-1999

C:Accession: A26158

R:Padgett, R.W.; St. Johnston, R.D.; Gelbart, W.M.

Nature 325, 81-84, 1987

A:Title: A transcript from a Drosophila pattern gene predicts a protein homologous to ti

A:Reference number: A26158; MUID:87090408; PMID:3467201

A:Accession: A26158

A:Molecule type: mRNA

A:Residues: 1-588 <PAD>

A:Cross-references: GB:M30116; NID:9157291; PID:9157292

C:Genetics:

A:Gene: FlyBase:dp

A:Cross-references: FlyBase:FBgn0000490

C:Keywords: glycoprotein

F:1-15/Domain: signal sequence #status predicted <SIG>

F:120,342,377,529/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match

Best Local Similarity 53.0%; Score 344; DB 2; Length 588;

Matches 57; Conservative 24; Mismatches 34; Indels 2; Gaps 1;

QY

5 RGRGRPS-KRLKARCSRKALHVNFKMGMDWIIAPLEYAFHCEGLCEFPRLRSH 62

DB 472 RHARRSPRRKKNKCRHSLYVDFSDVGMNDWIVAPPGYQAFYCHGDCPEPLADHFNST 531

QY

63 NHAIVQTLNMSMDPESTPTACVPTRLSPISILFIDSANNVYQYEDMYESGCG 119

DB 532 NHAIVQTLNMSMDPESTPTACVPTRLSPISILFIDSANNVYQYEDMYESGCG 588

QY

DB

QY

DB

QY

DB

QY

DB

QY

bone morphogenetic protein 211 precursor - African clawed frog

C:Species: Xenopus laevis (African clawed frog)

C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Jul-1999

C:Accession: JH0688

R:Nishimatsu, S.; Suzuki, A.; Shoda, A.; Murakami, K.; Ueno, N.

Biochem. Biophys. Res. Commun. 186, 1487-1495, 1992

A>Title: Genes for bone morphogenetic proteins are differentially transcribed in early a

A:Reference number: JH0687; MUID:92378616; PMID:1510675

A:Accession: JH0688

A:Molecule type: mRNA

A:Residues: 1-398 <NIS>

A:Cross-references: GB:X63425; NID:964583; PIDN:CAA45019.1; PID:964584

A:Experimental source: oocyte

C:Superfamily: inhibin

C:Keywords: glycoprotein

F:285-398/Product: bone morphogenetic protein 211 #status predicted <Mat>

F:137,202,237,340/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 52.9%; Score 343; DB 2; Length 398;

Best Local Similarity 53.4%; Pred. No. 7,6e-28;

Matches 62; Conservative 19; Mismatches 33; Indels 2; Gaps 2;

QY 5 RQCK-RPSKRLKRCGRKALHNFKMGWDDMTIAPLEYAFHCEGLCEPRLRSHLEPTN 63

DB 284 RQARRKQRRRLKSSCRHPLYVDSVGMNDWIAPPGYHAPYCHGECPPPLADHLNSTN 343

QY 64 HAVICTINMSMDPESTPTACVPTRLSPISILFIDSANNVYKQYEDMVVESGGR 119

DB 344 HAVIQTIVNSV-N-TNTPKACCVPTELSAISMLYLDENENKVAKNYQDMVVEGCGCR 398

Search completed: February 18, 2004, 17:43:53

Job time : 21 secs

RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
 RA Whitehead S.L., Whitaker P., Willey D.L., Williams L., Williams S.A.,
 RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
 RA Rogers J.;
 RT "The DNA sequence and comparative analysis of human chromosome 20.";
 RL Nature 414:865-871 (2001).
 RN (4)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse J.H., Derge J.G.,
 RA Altshuler R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeng B., Buetow K.H., Schaefer C.F., Bat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusik A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Iqbal N.A., Peters G.J., Abramson R.D., Mallory S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Villalón D.K., Muzny K.C., Hale S., Garcia A.M., Gay L.V., Hultk S.W.,
 RA Richardson S., Morley K.C., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Watkins R.W., Touchman J.W., Green E.D., Dickinson M.C.,
 RA Blakesley A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Rodriguez Y.S.N., Krzywicki M.I., Skaleka U., Smallos D.E.,
 RA Scherch A., Schein U.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 CC -1- FUNCTION: COULD BE INVOLVED IN BONE FORMATION.
 CC -1- SUBUNIT: Homodimer; disulfide-linked (by similarity).
 CC -1- TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN LONG BONES DURING
 CC HUMAN EMBRYONIC DEVELOPMENT.
 CC -1- DISEASE: DEFECTS IN GDF5 ARE A CAUSE OF ACROSMELIC
 CC CHONDRODYSPLASIA OF THE HUNTER-THOMPSON TYPE. THIS FORM OF
 CC DWARFISM IS CHARACTERIZED BY SHORT FOREARMS, HANDS AND FEET. THE
 CC RADIIUS IS CURVED AND ITS HEAD IS OFTEN DISLOCATED POSTERIORLY. THE
 CC METACARPALS, METATARSALS AND PHALANGES ARE PARTICULARLY SHORT. THE
 CC PHALANGES ARE ALMOST SQUARE.
 CC -1- SIMILARITY: Belongs to the TGF-beta family.
 CC -----
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 CC -----
 DR EMBL; X80915; CAA56874.1; -;
 DR EMBL; U13660; AAB57007.1; -;
 DR EMBL; AL121586; CAB89416.1; -;
 DR EMBL; BC032495; AAB32495.1; -;
 DR PIR; A55452; A55452.
 DR PIR; JC2347; JC2347.
 DR HSSP; P12643; 3BMP.
 DR Genew; HGNC:4220; GDF5.
 DR MIM; 601146; -;
 DR MIM; 201250; -;
 DR MIM; 200700; -;
 DR GO; GO:0008083; F: growth factor activity; TAS.
 DR GO; GO:0005515; F: protein binding activity; TAS.
 DR GO; GO:0007267; P: cell-cell signaling; TAS.
 DR GO; GO:0007179; P: TGF-beta receptor signaling pathway; TAS.
 DR InterPro; IPR001839; TGFb_N.
 DR InterPro; IPR001111; TGFb_N.
 DR Pfam; PF00688; TGFb_propeptide; 1.
 DR Pfam; PF000357; TGFb; 1.
 DR SMART; SM00204; TGFb; 1.
 DR PROSITE; PS00250; TGF_beta_1; 1.
 DR Signal; Growth factor; Cytokine; Glycoprotein; Dwarfism.

FT SIGNAL 1 27
 FT PROPEP 28 381
 FT CHAIN 382 501
 FT DISULFID 400 466
 FT DISULFID 429 498
 FT DISULFID 433 500
 FT DISULFID 465 465
 FT CARBOHYD 189 189
 FT CONFLICT 38 38
 FT CONFLICT 254 258
 FT CONFLICT 276 276
 FT CONFLICT 321 321
 FT CONFLICT 384 384
 SQ SEQUENCE 501 AA; 55410 MW; 37985F2D15C4F5ER CRC64;
 Query Match 99.4%; Score 645; DB 1; Length 501;
 Best Local Similarity 99.2%; Pred. No. 1.2e-61;
 Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 PLATROGKRPENKTKARCSKALHVFDMGMDWMTAELVEAFHCGLCPEPLRSHLE 60
 DB 383 PLATROGKRPENKTKARCSKALHVFDMGMDWMTAELVEAFHCGLCPEPLRSHLE 442
 QY 61 PTHNAVICTLNMNSMDPESTPTACVPTLSPISILFIDSNANVYKQYEDMVESCGGR 119
 DB 443 PTHNAVICTLNMNSMDPESTPTACVPTLSPISILFIDSNANVYKQYEDMVESCGGR 501
 RESULT 2
 GDF5_MOUSE STANDARD; PRT; 495 AA.
 ID ID P43027;
 AC 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Growth/differentiation factor 5 precursor (GDF-5).
 GN GDF5 OR GDF-5 OR BF.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CD-1; TISSUE=Embryo;
 RX MEDLINE=94195427; PubMed=8145850;
 RA Storm E.E., Huynh T.V., Copeland N.G., Jenkins N.A., Kingsley D.M.,
 RA Lee S.-U.;
 RT "Limb alterations in brachypodism mice due to mutations in a new
 RT member of the TGF beta-superfamily.";
 RL Nature 368:639-643 (1994).
 CC -1- FUNCTION: COULD BE INVOLVED IN BONE FORMATION.
 CC -1- SUBUNIT: Homodimer; disulfide-linked (by similarity).
 CC -1- DISEASE: DEFECTS IN GDF5 ARE THE CAUSE OF BRACHYPODISM WHICH
 CC ALTERS THE LENGTH AND NUMBERS OF BONES IN THE LIMBS BUT SPARES THE
 CC AXIAL SKELETON.
 CC -1- SIMILARITY: Belongs to the TGF-beta family.
 CC -----
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 CC -----
 DR EMBL; U08337; AAA18778.1; -;
 DR PIR; S43294; S43294.
 DR HSSP; P12643; 3BMP.
 DR MGD; MGI:95688; Gdf5.
 DR InterPro; IPR001839; TGFb_N.
 DR InterPro; IPR001111; TGFb_N.
 DR Pfam; PF00688; TGFb_propeptide; 1.

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DR PRODOM; PD000357; TGFβ; 1.
DR SMART; SM00204; TGFβ; 1.
DR PROSITE; PS00250; TGFβ; 1.
KW SIGNAL; Growth factor; Cytokine; Glycoprotein; Polymorphism.
FT SIGNAL 1 27
FT PROPEP 28 375
FT CHAIN 376 495
FT DISULFID 394 460
FT DISULFID 423 492
FT DISULFID 427 494
FT DISULFID 459 459
FT CARBOHYD 183 183
FT VARIANT 98 98
SQ SEQUENCE 495 AA; 54885 MW; CD05DE48185DE3 CRC64;

Query Match
Best Local Similarity 98.3%; Score 640; DB 1; Length 495;
Matches 117; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 PLATROCKRPSKRLKARCSKRLALVNFKMGMDWIIAPLEYEAFHCEGHCPEPLRSHTLE 60
DB 377 PLNRQGRPSKRLKARCSKRLALVNFKMGMDWIIAPLEYEAFHCEGHCPEPLRSHTLE 436
QY 61 PTHNAVITLNMNDPESTPTACVPTLSPISILFIDSANNVYKQYEDMVESGCR 119
DB 437 PTHNAVITLNMNDPESTPTACVPTLSPISILFIDSANNVYKQYEDMVESGCR 495

RESULT 3
GDF6_MOUSE STANDARD; PRT; 125 AA.
ID GDF6_MOUSE
AC P43028;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Growth/differentiation factor 6 precursor (GDF-6) (Fragment).
GN GDF6 OR GDF-6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BAIB/c; TISSUE=Liver;
RX MEDLINE=94195427; PubMed=8145850;
RA Storm E.E., Hyman T.V., Copeland N.G., Jenkins N.A., Kingsley D.M.,
RA Lee S.-J.;
RT "Limb alterations in brachypodism mice due to mutations in a new
RT member of the TGF beta-superfamily."
RL Nature 368:639-643 (1994).
CC -1 SUBUNIT: Homodimer; disulfide-linked (By similarity).
CC -1 SIMILARITY: Belongs to the TGF-beta family.
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; U08338; AAA18779.1; -.
CC PIR; S43295; S43295.
CC HSSP; P12643; 3BMP.
CC MGD; MGI:95689; Gdf6.
CC InterPro; IPR002400; GF_cysknot.
CC InterPro; IPR002405; Inhibin_alpha.
CC InterPro; IPR001839; TGFβ.
CC Pfam; PF00019; TGF-beta; 1.
CC Pfam; PF00868; GFCYSKNOT.
CC PRINTS; PR00669; INHIBINA.
CC SMART; SM00357; TGFβ; 1.
CC PRODOM; PD000357; TGFβ; 1.
CC SMART; SM00204; TGFβ; 1.

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DR PROSITE; PS00250; TGFβ; 1.
KW Growth factor; Cytokine; Glycoprotein.
FT NON TER 1 5
FT PROPEP <1 125
FT CHAIN 6 125
FT DISULFID 24 90
FT DISULFID 53 122
FT DISULFID 57 124
FT DISULFID 89 89
SQ SEQUENCE 125 AA; 14373 MW; 10FA2A5B7748DA32 CRC64;

Query Match
Best Local Similarity 83.7%; Score 543; DB 1; Length 125;
Matches 94; Conservative 13; Mismatches 10; Indels 0; Gaps 0;

QY 3 ACTROGKRPSPKRLKARCSKRLALVNFKMGMDWIIAPLEYEAFHCEGHCPEPLRSHTLEPT 62
DB 9 ASRHGRHGRKSRRLRSKRLALVNFKMGMDWIIAPLEYEAFHCEGHCPEPLRSHTLEPT 68
QY 63 NNAVITLNMNDPESTPTACVPTLSPISILFIDSANNVYKQYEDMVESGCR 119
DB 69 NNAVITLNMNDPESTPTACVPTLSPISILFIDSANNVYKQYEDMVESGCR 125

RESULT 4
GDF6_BOVIN STANDARD; PRT; 436 AA.
ID GDF6_BOVIN
AC P55106;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Growth/differentiation factor 6 precursor (GDF-6) (Cartilage-derived
DE morphogenetic protein 2) (CDMP-2) (Fragment).
GN GDF6 OR CDMP2.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Articular cartilage;
RX MEDLINE=95050604; PubMed=7961761;
RA Chang S., Hoang B., Thomas V.T., Vukicevic S., Luyten F.P.,
RA Ryba N.J.P., Kozak C.A., Reddi A.H., Woods M.;
RT "Cartilage-derived morphogenetic proteins. New members of the
RT transforming growth factor-beta superfamily predominantly expressed
RT in long bones during human embryonic development."
RL J. Biol. Chem. 269:28227-28234 (1994).
CC -1 SUBUNIT: Homodimer; disulfide-linked (By similarity).
CC -1 SIMILARITY: Belongs to the TGF-beta family.
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; U13661; AAA61416.1; -.
CC PIR; B55452; B55452.
CC HSSP; P18075; 1BMP.
CC InterPro; IPR002400; GF_cysknot.
CC InterPro; IPR001839; TGFβ.
CC InterPro; IPR001111; TGFβ_N.
CC Pfam; PF00019; TGF-beta; 1.
CC Pfam; PF00868; TGFβ_propeptide; 1.
CC PRINTS; PR00438; GFCYSKNOT.
CC SMART; SM00357; TGFβ; 1.
CC SMART; SM00204; TGFβ; 1.
CC PROSITE; PS00250; TGFβ; 1.
CC Growth factor; Cytokine; Glycoprotein.

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FT  NON TER      1      1
FT  PROPEP      <1      316      POTENTIAL.
FT  CHAIN      317      436      GROWTH/DIFFERENTIATION FACTOR 6.
FT  DISULFID    335      401      BY SIMILARITY.
FT  DISULFID    364      433      BY SIMILARITY.
FT  DISULFID    368      435      BY SIMILARITY.
FT  DISULFID    400      400      INTERCHAIN (BY SIMILARITY).
FT  CARBOHYD    27      27      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT  CARBOHYD    89      89      N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ  SEQUENCE      436 AA; 47873 MW; B06888E12F8A91D CRC64;

Query Match
Best Local Similarity 76.9%; Score 528; DB 1; Length 436;
Matches 90; Conservative 16; Mismatches 11; Indels 0; Gaps 0;

QY  3  ATRGKRPKSKLKARCSKRALHVNFKMGMDMTIAPLFEYAFHCEGLCEPFLRSHLEPT 62
    1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
    1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db  320 ASHGKRGKSKRLRCSKPLHVNFKELGMDMTIAPLFEYAFHCEGLCEPFLRSHLEPT 379
    1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
    1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1

QY  63  NNAVITLNNMSPDEPTACVPTLSPISILFDSANNVYKQYEDMVVSCGCR 119
    1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
    1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db  380 NNAITQLNMSMDPGSTPPSCVPTKLTPLISILYIDANNVYNEYEENWVSCGCR 436
    1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
    1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1

RESULT 5
GDF7_MOUSE
ID  GDF7_MOUSE      STANDARD;      PRT;      151 AA.
AC  P43029;
DT  01-NOV-1995 (Rel. 32, Created)
DT  01-NOV-1995 (Rel. 32, Last sequence update)
DT  16-OCT-2001 (Rel. 40, Last annotation update)
DE  Growth/differentiation factor 7 precursor (GDF-7) (Fragment).
GN  GDF7 OR GDF-7.
OS  Mus musculus (Mouse).
OC  Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC  NCBI_TaxID=10090;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=BALB/c; TISSUE=Liver;
RA  MEDLINE=94195427; Pubmed=8145850.
RA  Storm E.R., Huyah T.V., Copeland N.G., Jenkins N.A., Kingsley D.M.,
RA  Lee S.-J.;
RT  "Limb alterations in brachypodism mice due to mutations in a new
RT  member of the TGF beta-superfamily.";
RL  Nature 368:639-643(1994).
CC  -1- SUBUNIT: Homodimer; disulfide-linked (By similarity).
CC  -1- SIMILARITY: Belongs to the TGF-beta family.
CC  -----
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CC  or send an email to license@isb-sib.ch).
CC  -----
CC  EMBL; U08339; AAA18780.1; -.
CC  PIR; S43296; S43296.
DR  HSSP; P12643; 3BMP.
DR  MCD; MGI:95690; Gdf7.
DR  InterPro; IPR002400; GE_cyknknot.
DR  InterPro; IPR001839; TGFb.
DR  Pfam; PF00019; TGF-beta.1.
DR  PRINTS; PR00438; GFCYSKNOT.
DR  PRODOM; PD000357; TGFb.1.
DR  SMART; SM00204; TGFb.1.
DR  PROSITE; PS00250; TGF_BETA_1; 1.
KW  Growth factor; Cytokine; Glycoprotein.
FT  NON TER      1      1
FT  PROPEP      <1      5      POTENTIAL.
FT  CHAIN      6      151      GROWTH/DIFFERENTIATION FACTOR 7.
FT  DISULFID    50      116      BY SIMILARITY.

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FT  DISULFID    79      148      BY SIMILARITY.
FT  DISULFID    83      150      BY SIMILARITY.
FT  DISULFID    115      115      INTERCHAIN (BY SIMILARITY).
FT  DOMAIN      1      5      POLY-ARG.
FT  DOMAIN      16      41      POLY-GLX.
SQ  SEQUENCE      151 AA; 15697 MW; 0B496ACB5827759 CRC64;

Query Match
Best Local Similarity 73.5%; Score 493; DB 1; Length 151;
Matches 83; Conservative 20; Mismatches 10; Indels 0; Gaps 0;

QY  7  GKRPSPKIKAKCSKRALHVNFKMGMDMTIAPLFEYAFHCEGLCEPFLRSHLEPTNNAV 66
    1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
    1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db  39  GRGGRGRGRGRSKSLHVDKELGMDMTIAPLFEYAFHCEGLCEPFLRSHLEPTNNAI 98
    1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
    1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1

QY  67  IOTLNNMSPDEPTACVPTLSPISILFDSANNVYKQYEDMVVSCGCR 119
    1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
    1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db  99  IOTLNNMSPDEPTACVPTLSPISILYIDANNVYKQYEDMVVSCGCR 151
    1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
    1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1

RESULT 6
DVR1_STRPU
ID  DVR1_STRPU      STANDARD;      PRT;      461 AA.
AC  P48969;
DT  01-FEB-1996 (Rel. 33, Created)
DT  01-FEB-1996 (Rel. 33, Last sequence update)
DT  16-OCT-2001 (Rel. 40, Last annotation update)
DE  DVR-1 protein homolog precursor.
GN  DVR1.
OS  Strongylocentrotus purpuratus (Purple sea urchin).
OC  Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC  Echinoidea; Echinoidea; Echinacea; Echinoida; Strongylocentrotidae;
OC  Strongylocentrotus.
OC  NCBI_TaxID=7668;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  Ponce M.R., Macol J.L., Davidson E.H.;
RL  Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.
CC  -1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (PROBABLY).
CC  -1- SIMILARITY: Belongs to the TGF-beta family.
CC  -----
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CC  -----
CC  EMBL; Z48313; CAA88306.1; -.
CC  PIR; S52408; S52408.
DR  HSSP; P18075; 1BMP.
DR  InterPro; IPR002405; Inhibin_alpha.
DR  InterPro; IPR001839; TGFb.
DR  InterPro; IPR001111; TGFb_N.
DR  Pfam; PF00019; TGF-beta.1.
DR  Pfam; PF00668; TGFb_propeptide.1.
DR  PRINTS; PR00669; INHIBINA.
DR  PRODOM; PD000357; TGFb.1.
DR  SMART; SM00204; TGFb.1.
DR  PROSITE; PS00250; TGF_BETA_1; 1.
KW  Growth factor; Cytokine; Glycoprotein; Signal.
FT  SIGNAL      1      30      POTENTIAL.
FT  PROPEP      31      338      POTENTIAL.
FT  CHAIN      339      461      DVR-1 PROTEIN HOMOLOG.
FT  DISULFID    360      426      BY SIMILARITY.
FT  DISULFID    389      458      BY SIMILARITY.
FT  DISULFID    393      460      BY SIMILARITY.
FT  DISULFID    425      425      INTERCHAIN (BY SIMILARITY).
FT  DISULFID    449      449      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT  CARBOHYD    402      402      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT  CARBOHYD    461 AA; 51881 MW; 2573D54B625F7BF CRC64;
SQ  SEQUENCE

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Query Match          54.5%; Score 353.5; DB 1; Length 461;
Best Local Similarity 48.1%; Pred. No. 2.1e-30;
Matches 65; Conservative 19; Mismatches 32; Indels 19; Gaps 2;

QY 3 ATRO---GKPPSK-----NIKARCSKALHVNFKMGMDWITAPLEYE 43
DB 326 ATROCKGKGGKPRKEDTNDNDIASRDSASSLNSDWCKKRNLFVNFEDIDWQEWIIAPAGYV 385

QY 44 AFHCEGICEPPLRSHLPTTHAVIQTLMSNDPESTPTACVPTRLSPISILFTDSANNV 103
DB 386 AFYQGGCAPPPLNGHANAHAIVQTLVHMSPEHVPQPCAPTKLSPTIVLYDDSRNV 445

QY 104 VYKQYEDMVVESCSCG 118
DB 446 VLKYYKMMVVRACGC 460

RESULT 7
UNIT STRPU STANDARD; PRT; 395 AA.
AC P48970;
DT 01-FEB-1996 (Rel. 33, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Univin precursor.
OS Strongylocentrotus purpuratus (Purple sea urchin).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinoidae; Euechinoidae; Echinacea; Echinoida; Strongylocentrotidae;
OC Strongylocentrotus.
OX NCBI_TaxID=7668;
RN SEQUENCE FROM N.A.
RX MEDLINE=95046997; PubMed=7958442;
RA Stenzel P., Angerer L.M., Smith B.J., Angerer R.C., Vale W.W.;
RT "The univin gene encodes a member of the transforming growth
RT factor-beta superfamily with restricted expression in the sea urchin
RT embryo."
RL Dev. Biol. 166:149-158 (1994).
RN
RP REVISIONS TO N-TERMINUS.
RA Angerer L.M., Stenzel P.;
RL Submitted (Oct-2000) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: COULD HAVE A CRITICAL ROLE IN EARLY DEVELOPMENTAL
CC DECISIONS IN THE SEA URCHIN EMBRYO.
CC -1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (PROBABLY).
CC -1- DEVELOPMENTAL STAGE: HIGHEST LEVELS OF EXPRESSION IN THE EGG AND
CC PRONANCHED BLASTULA. DURING LATE CLEAVAGE STAGES, IT ACCUMULATES
CC PROGRESSIVELY TO A CIRCUMCUMTORIAL BAND. DURING GASTRULATION IT
CC IS DETECTED PRIMARILY IN THE PRESUMPTIVE FOREGUT AND CILIATED
CC BAND. BY PLUTEUS STAGE, IT IS DETECTED ONLY IN THESE CELL TYPES.
CC -1- SIMILARITY: Belongs to the TGF-beta family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL, U10533; AA57553.2; -.
DR HSSP; P12643; 3BMP.
DR InterPro; IPR001839; TGFb.
DR InterPro; IPR001111; TGFb N.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGFb propeptide; 1.
DR PfDom; PD000357; TGFb; 1.
DR SMART; SM00204; TGFb; 1.
DR PROSITE; PS00250; TGF_BETA_1; 1.
DR Growth factor; Cytokine; Glycoprotein; Signal.
KM SIGNAL 1 19
FT SIGNAL 20 272
FT PROPEP 273 395
FT CHAIN 273 395
FT UNIVIN.

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FT DISULFID 294 360 BY SIMILARITY.
FT DISULFID 323 392 BY SIMILARITY.
FT DISULFID 327 394 BY SIMILARITY.
FT DISULFID 359 359 INTERCHAIN (BY SIMILARITY).
FT CARBOHYD 50 50 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 116 116 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 336 336 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 395 AA; 43837 MW; 0FA340DF5A360E CRC64;

Query Match          54.2%; Score 352; DB 1; Length 395;
Best Local Similarity 48.1%; Pred. No. 2.5e-30;
Matches 60; Conservative 22; Mismatches 28; Indels 0; Gaps 0;

QY 10 PSXNLKARCSKALHVNFKMGMDWITAPLEYEAHCBSGCEPPLRSHLPTTHAVIQ 69
DB 286 PTASLTNLCQRRHLTFVSPFDVGMENWIIAPMGYQAYCYDCEPPLGERLNGTTHAVIQ 345

QY 70 LMSNDPESTPTACVPTRLSPISILFTDSANNVYKQYEDMVVESCSCG 119
DB 346 LVNSIDNRAVVKVCAPTKLSISMLYFDNNENVVLRYEDMVVAVACGCR 395

RESULT 8
BMP2_RAT STANDARD; PRT; 393 AA.
ID BMP2_RAT
AC P49001;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Bone morphogenetic protein 2 precursor (BMP-2) (BMP-2A).
GN BMP2 OR BMP-2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX Feng J.Q., Chen D., Feng M., Harris M.A., Mundy G.R., Harris S.E.;
RC TISSUE=Bone;
RA Submitted (SEP-1993) to the EMBL/GenBank/DBJ databases.
RL -1- FUNCTION: INDUCES CARTILAGE AND BONE FORMATION.
CC -1- SUBUNIT: Homodimer; disulfide-linked.
CC -1- TISSUE SPECIFICITY: FEMUR, CALVARIA, TRACHEA, LUNG AND OVARY.
CC -1- SIMILARITY: Belongs to the TGF-beta family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; Z25868; CAA81088.1; -.
DR PIR; S37073; S37073.
DR HSSP; P12643; 3BMP.
DR InterPro; IPR002405; Inhibin_alpha.
DR InterPro; IPR001839; TGFb.
DR InterPro; IPR001111; TGFb N.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGFb propeptide; 1.
DR PRINTS; PR00669; INHIBINA.
DR PRODOM; PD000357; TGFb; 1.
DR SMART; SM00204; TGFb; 1.
DR PROSITE; PS00250; TGF_BETA_1; 1.
DR Growth factor; Cytokine; Bone; Cartilage; Glycoprotein.
KM SIGNAL 1 19
FT PROPEP 20 279
FT CHAIN 280 393
FT DISULFID 293 358 BY SIMILARITY.
FT DISULFID 322 390 BY SIMILARITY.
FT DISULFID 326 392 BY SIMILARITY.
FT DISULFID 357 357 INTERCHAIN (BY SIMILARITY).

```

FT CARBOHYD 133 133 N-LINKED (GLCNAC. . .) (POTENTIAL)
 FT CARBOHYD 161 161 N-LINKED (GLCNAC. . .) (POTENTIAL)
 FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .) (POTENTIAL)
 FT CARBOHYD 335 335 N-LINKED (GLCNAC. . .) (POTENTIAL)
 SQ SEQUENCE 393 AA; 44383 MW; 7D20865852E0F213 CRC64;

Query Match 53.5%; Score 347; DB 1; Length 393;
 Best Local Similarity 54.3%; Pred. No. 8.7e-30;
 Matches 63; Conservative 17; Mismatches 34; Indels 2; Gaps 2;

QY 5 RQK-RPSNKLKARCSRKALHVFQKMGDDMTIAPLEYAHPCHGLCEPPLRSHLEPTN 63
 DB 279 RQKHQRKRLKSSCKRHPLYVDFSDVGWMDMTVAPPGYHAFYCHGECPPLADHLNSTN 338
 QY 64 HAVIOTLMSMDPESTPPACVPTPLSPISLIFDSANNVVKQYEDMVEGCGR 119
 DB 339 HAVIOTLVMSVN-SKIPKACVPTPLSMTLIDENEKVKLNQYDMVVEGCGR 393

RESULT 9

BMP2_MOUSE STANDARD; PRT; 394 AA.

AC F21274;
 DT 01-MAY-1991 (Rel. 18, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Bone morphogenetic protein 2 precursor (BMP-2) (BMP-2A).
 GN BMP2 OR BMP-2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94289485; PubMed=8018727;
 RA Feng J.Q., Harris M.A., Ghosh-Choudhury N., Feng M., Murdy G.R.,
 RA Harris S.E.;
 RT "Structure and sequence of mouse bone morphogenetic protein-2 gene
 (BMP-2): comparison of the structures and promoter regions of BMP-2
 RT and BMP-4 genes.";
 RL Biochim. Biophys. Acta 1218:221-224 (1994).
 RN [2]
 RP SEQUENCE OF 1-351 FROM N.A.
 RX MEDLINE=90228966; PubMed=1970330;
 RA Dickinson M.E., Kobrin M.S., Silan C.M., Kingsley D.M., Justice M.J.,
 RA Miller D.A., Cecil J.D., Lock L.F., Lee A., Buchberg A.M.,
 RA Stracusa L.D., Lyons K.M., Derynck R., Hogan B.L.M., Copeland N.G.,
 RA Jenkins N.A.;
 RT "Chromosomal localization of seven members of the murine TGF-beta
 RT superfamily suggests close linkage to several morphogenetic mutant
 RT loci";
 RL Genomics 6:505-520 (1990).

CC -1- FUNCTION: INDUCES CARTILAGE AND BONE FORMATION.
 CC -1- SUBUNIT: Homodimer; disulfide-linked.
 CC -1- SIMILARITY: Belongs to the TGF-beta family.
 CC -----
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CC -----
 CC EMBL: L25602; AAB05665.1; -
 CC PIR: A34201; A34201.
 CC HSSP: P12643; 3BMP.
 CC GSD; MGI:88177; BMP2.
 CC GO: GO:0045165; P:cell fate commitment; IMP.
 CC GO: GO:0009790; P:embryonic development; IMP.
 CC GO: GO:0009887; P:organogenesis; IMP.
 CC InterPro: IPR001839; TGFb.
 CC InterPro: IPR001111; TGFb_N.

DR PFam; PF00019; TGF-beta; 1.
 DR Pfam; PF00688; TGFb propeptide; 1.
 DR ProDom; PD000357; TGFb; 1.
 DR SMART; SM00204; TGFb; 1.
 DR PROSITE; PS00250; TGF_BETA_1; 1.
 KW Signal; Growth factor; Cytokine; Bone; Cartilage; Glycoprotein.
 FT SIGNAL 1
 FT PROPEP 20 280
 FT CHAIN 281 394
 FT DISULFID 281 394
 FT DISULFID 323 391
 FT DISULFID 327 393
 FT DISULFID 358 358
 FT CARBOHYD 134 134
 FT CARBOHYD 162 162
 FT CARBOHYD 198 198
 FT CARBOHYD 336 336
 FT CARBOHYD 336 336
 FT CONFLICT 110 110
 FT CONFLICT 113 114
 FT CONFLICT 113 114
 FT CONFLICT 271 271
 SQ SEQUENCE 394 AA; 44514 MW; FDEA0F10587ED54 CRC64;

Query Match 53.5%; Score 347; DB 1; Length 394;
 Best Local Similarity 54.3%; Pred. No. 8.7e-30;
 Matches 63; Conservative 17; Mismatches 34; Indels 2; Gaps 2;

QY 5 RQK-RPSNKLKARCSRKALHVFQKMGDDMTIAPLEYAHPCHGLCEPPLRSHLEPTN 63
 DB 280 RQKHQRKRLKSSCKRHPLYVDFSDVGWMDMTVAPPGYHAFYCHGECPPLADHLNSTN 339
 QY 64 HAVIOTLMSMDPESTPPACVPTPLSPISLIFDSANNVVKQYEDMVEGCGR 119
 DB 340 HAVIOTLVMSVN-SKIPKACVPTPLSMTLIDENEKVKLNQYDMVVEGCGR 394

RESULT 10

BMP2_RABBIT STANDARD; PRT; 395 AA.

AC O46564;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Bone morphogenetic protein 2 precursor (BMP-2).
 GN BMP2 OR BMP-2.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=New Zealand white; TISSUE=Ocular ciliary epithelium;
 RA Wan X.L., Sears J., Chen S., Sears M.;
 RT "Cloning and expression of BMP-2/-4 from rabbit ocular ciliary
 RT epithelium";
 RL Submitted (JAN-1998) to the EMBL/GenBank/DDA databases.

CC -1- FUNCTION: INDUCES CARTILAGE AND BONE FORMATION (BY SIMILARITY).
 CC -1- SUBUNIT: Homodimer; disulfide-linked (By similarity).
 CC -1- SIMILARITY: Belongs to the TGF-beta family.
 CC -----
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CC -----
 CC EMBL: AF041421; AAB96785.1; -
 CC HSSP: P12643; 3BMP.
 CC InterPro: IPR002405; Inhibin_alpha.
 CC InterPro: IPR001839; TGFb.
 CC InterPro: IPR001111; TGFb_N.
 CC Pfam; PF00019; TGF-beta; 1.

DR PFam; PF00019; TGF-beta; 1.
 DR Pfam; PF00688; TGFb propeptide; 1.
 DR ProDom; PD000357; TGFb; 1.
 DR SMART; SM00204; TGFb; 1.
 DR PROSITE; PS00250; TGF_BETA_1; 1.
 KW Signal; Growth factor; Cytokine; Bone; Cartilage; Glycoprotein.
 FT SIGNAL 1
 FT PROPEP 20 280
 FT CHAIN 281 394
 FT DISULFID 281 394
 FT DISULFID 323 391
 FT DISULFID 327 393
 FT DISULFID 358 358
 FT CARBOHYD 134 134
 FT CARBOHYD 162 162
 FT CARBOHYD 198 198
 FT CARBOHYD 336 336
 FT CARBOHYD 336 336
 FT CONFLICT 110 110
 FT CONFLICT 113 114
 FT CONFLICT 113 114
 FT CONFLICT 271 271
 SQ SEQUENCE 394 AA; 44514 MW; FDEA0F10587ED54 CRC64;

DR Pfam; PF00688; TGFb_propeptide; 1.
 DR PRINTS; PR00669; INHIBIN.
 DR PRODOM; PD000357; TGFb; 1.
 DR SMART; SM00204; TGFb; 1.
 DR PROSITE; PS00250; TGF_BETA_1; 1.
 DR Signal; Growth factor; Cytokine; Bone; Cartilage; Glycoprotein.
 KW Signal; Growth factor; Cytokine; Bone; Cartilage; Glycoprotein.
 FT SIGNAL 1 23
 FT PROPEP 1 24
 FT CHAIN 282 281
 FT DISULFID 295 360
 FT DISULFID 324 392
 FT DISULFID 328 394
 FT DISULFID 359 394
 FT CARBOHYD 134 134
 FT CARBOHYD 199 199
 FT CARBOHYD 337 337
 SQ SEQUENCE 395 AA; 44664 MW; 8D1DCFBAC582496 CRC64;
 Query Match 53.5%; Score 347; DB 1; Length 395;
 Best local Similarity 54.3%; Pred. No. 8.8e-30;
 Matches 63; Conservative 17; Mismatches 34; Indels 2; Gaps 2;
 QY 5 RQCK-RPSKNLRCRCRKALHVNFKMGMDMIIAPLEYAFHCEGLCEPPLASHLEPTN 63
 DB 281 RQAKHKQRKLKSSCKRHPLYVDFSDVGNMDWVAEPGYHAFYCHGECPPPLADHINSTN 340
 QY 64 HAVIQTLMNSMDESPPTACVPRRLSPISILFIDSANNVVKQYEDMVESGCCR 119
 DB 341 HAVIQTLMNSVN-SKIPKACCVPTLSALSMYLIDENEKVKLVKNYQDMVVEGGCCR 395

RESULT 11
 BMP2_DAMDA
 ID BMP2_DAMDA STANDARD; PRT; 396 AA.
 AC 019006;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Bone morphogenetic protein 2 precursor (BMP-2).
 GN BMP2.
 OS Dama dama (Fallow deer) (Cervus dama).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidae;
 OC Cervidae; Cervinae; Cervus.
 OX NCBI_Taxid=30532;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Antler;
 RX MEDLINE=97157076; PubMed=9003457;
 RA Feng J.Q., Chen D., Ghosh-Choudhury N., Esparza J., Mundy G.R.,
 RA Harris S.E.;
 RT "Bone morphogenetic protein 2 transcripts in rapidly developing deer
 RT antler tissue contain an extended 5' non-coding region arising from a
 RT distal promoter";
 RL Biochim. Biophys. Acta 1350:47-52(1997).
 CC -1- FUNCTION: INDUCES CARTILAGE AND BONE FORMATION.
 CC -1- SUBUNIT: Homodimer; disulfide-linked.
 CC -1- SIMILARITY: Belongs to the TGF-beta family.
 CC -----
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 CC -----
 CC EMBL; AJ001817; CAA05033.1; -
 CC HSSP; P12643; 3BMP.
 DR InterPro; IPR002405; Inhibin_alpha.
 DR InterPro; IPR001939; TGFb.
 DR InterPro; IPR001111; TGFb_N.
 DR Pfam; PF00019; TGF-beta; 1.

DR Pfam; PF00688; TGFb_propeptide; 1.
 DR PRINTS; PR00669; INHIBIN.
 DR PRODOM; PD000357; TGFb; 1.
 DR SMART; SM00204; TGFb; 1.
 DR PROSITE; PS00250; TGF_BETA_1; 1.
 DR Signal; Growth factor; Cytokine; Bone; Cartilage; Glycoprotein.
 KW Signal; Growth factor; Cytokine; Bone; Cartilage; Glycoprotein.
 FT SIGNAL 1 23
 FT PROPEP 1 24
 FT CHAIN 283 361
 FT DISULFID 296 361
 FT DISULFID 325 393
 FT DISULFID 329 395
 FT DISULFID 360 360
 FT CARBOHYD 135 135
 FT CARBOHYD 163 163
 FT CARBOHYD 164 164
 FT CARBOHYD 200 200
 FT CARBOHYD 338 338
 SQ SEQUENCE 396 AA; 44646 MW; 5FE23A0ACTF91572 CRC64;
 Query Match 53.5%; Score 347; DB 1; Length 396;
 Best local Similarity 54.3%; Pred. No. 8.8e-30;
 Matches 63; Conservative 17; Mismatches 34; Indels 2; Gaps 2;
 QY 5 RQCK-RPSKNLRCRCRKALHVNFKMGMDMIIAPLEYAFHCEGLCEPPLASHLEPTN 63
 DB 282 RQAKHKQRKLKSSCKRHPLYVDFSDVGNMDWVAEPGYHAFYCHGECPPPLADHINSTN 341
 QY 64 HAVIQTLMNSMDESPPTACVPRRLSPISILFIDSANNVVKQYEDMVESGCCR 119
 DB 342 HAVIQTLMNSVN-SKIPKACCVPTLSALSMYLIDENEKVKLVKNYQDMVVEGGCCR 396

RESULT 12
 BMP2_HUMAN
 ID BMP2_HUMAN STANDARD; PRT; 396 AA.
 AC P12643;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Bone morphogenetic protein 2 precursor (BMP-2) (BMP-2A).
 GN BMP2 OR BMP2A.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=89072730; PubMed=3201241;
 RX Wozney J.W., Rosen V., Celeste A.J., Mittleman B., Whitters M.J.,
 RA Kriz R.W., Hewick R.M., Wang E.A.;
 RT "Novel regulators of bone formation: molecular clones and
 RT activities";
 RL Science 242:1528-1534(1988).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Shore B.M., Xu M.-Q., Calvert G., Moricatis J., Kaplan F.S.;
 RT "Human bone morphogenetic protein 2 (BMP-2) genomic DNA sequence";
 RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21638749; PubMed=11780052;
 RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
 RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
 RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
 RA Beasley O.P., Bird C.P., Blake S.E., Bridgeman A.M., Brown A.J.,
 RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
 RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
 RA Clegg S., Cobley V.E., Collier R.B., Connor R.E., Corby N.R.,
 RA Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,
 RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
 RA Graham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
 RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,

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FT STRAND 302 304
FT TURN 305 309
FT TURN 311 313
FT STRAND 314 316
FT STRAND 319 321
FT STRAND 324 326
FT STRAND 328 328
FT TURN 331 332
FT STRAND 339 339
FT HELIX 341 352
FT TURN 354 355
FT STRAND 361 374
FT TURN 376 377
FT STRAND 380 396
SO SEQUENCE 396 AA; 44702 MW; 20653A3987B25B60 CRC64;

Query Match 53.5%; Score 347; DB 1; Length 396;
Best local Similarity 54.3%; Pred. No. 8.8e-30;
Matches 63; Conservative 17; Mismatches 34; Indels 2; Gaps 2;

Dy 5 RQGR-RRSKMLKRCRCRKLHVNPKMGWMDWIIAPLEFYAFPHOGLCEPFLRSHLPRTN 63
Db 282 RQAHKRRKRLKSKCRKRPVDFSDVGNMDWIAFPGYHAFYHGCPFLADHLNSTN 341
64 HAVIQTLMNSMDPESTPPACVPTRLSPISILFTDSANNVYKQYEDMVYSGCCR 119
342 HAVIQTLMNSVN-SKIPKACCVPELPSAISMLYDENEKRYVLKNYQDMVYEGCGCR 396

RESULT 13
EMP4_XENTIA STANDARD; PRT; 401 AA.
AC P30885;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Bone morphogenetic protein 4 precursor (BMP-4).
GN BMP-4 OR DVR-4.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodina; Xenopus.
OX NCBI_TaxID=8355;
[1]
RP SEQUENCE FROM N.A.
RN MEDLINE=92378616; PubMed=1510675;
RX Nishimatsu S., Suzuki A., Shoda A., Murakami K., Ueno N.;
RA "Genes for bone morphogenetic proteins are differentially transcribed
RT in early amphibian embryos.";
RL Biochem. Biophys. Res. Commun. 186:1487-1495 (1992).
[2]
RN CHARACTERIZATION.
RX MEDLINE=93048825; PubMed=1425343;
RA Jones C.M., Lyons K.M., Lapan P.M., Wright C.V., Hogan B.L.;
RT "DVR-4 (bone morphogenetic protein-4) as a posterior-ventralizing
RT factor in Xenopus mesoderm induction.";
RL Development 115:639-647(1992)
-1- INDUCTION. POSTERIOR-VENTRALIZING FACTOR IN XENOPUS MESODERM
INDUCTION. INDUCES POSTERIOVENTRAL MESODERM AND COUNTERACTS
-1- SUBUNIT: Homodimer; disulfide-linked (by similarity).
-1- SUBCELLULAR LOCATION: SECRETED INTO THE EXTRACELLULAR MATRIX.
-1- SIMILARITY: Belongs to the TGF-beta family.
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CC
DR EMBL; X63426; CAA45020.1; -.

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PIR: JH0689; JH0689.
 DR HSPF; P12643; 3BMP.
 DR InterPro; IPR001839; TGFb.
 DR InterPro; IPR001111; TGFb.N.
 DR Pfam; PF000019; TGF-beta; 1.
 DR Pfam; PF00688; TGFb_propeptide; 1.
 DR ProDom; PD000357; TGFb; 1.
 DR SMART; SM00204; TGFb; 1.
 DR SMART; SM00250; TGF_BETA_1; 1.
 DR Signal; Growth factor; Cytokine; Bone; Cartilage; Glycoprotein.
 KW SIGNAL.
 FT PROPEP 1 19
 FT CHAIN 20 287
 FT DISULFID 288 401
 FT DISULFID 301 366
 FT DISULFID 330 398
 FT DISULFID 334 400
 FT DISULFID 365 365
 FT CARBOHYD 141 141
 FT CARBOHYD 204 204
 FT CARBOHYD 238 238
 FT CARBOHYD 343 343
 FT CARBOHYD 358 358
 SQ SEQUENCE 401 AA; 45988 MW; 3580DEC4B990047 CRC64;

Query Match 53.5%; Score 347; DB 1; Length 401;
 Best Local Similarity 52.1%; Pred. No. 8.9e-30;
 Matches 63; Conservative 21; Mismatches 31; Indels 6; Gaps 2;

QY 4 TRQGRPSKLNKAR-----CSRKALHVFKDMGMDWMTIAPLEAEFHCGLCEPPLRSH 58
 DB 282 TRRKSPKQKPRKKNKCHRHSLYVDFSDVGNDWVAIPGQAFYCHDCCFPLADH 341
 QY 59 LEPTNAVITQTMNSMDEPSTPPACVPTLSPISIFISANNVYKQVEDMVESGCG 118
 DB 342 LNSTNHAIQVLTVNSVN-SSIPKACVPTLSISMILYIDYDKVLYKNQEMVVEGGCG 400
 QY 119 R 119
 DB 401 R 401

RESULT 14
 ID DECA_DROSI STANDARD; PRT; 593 AA.
 AC P91706;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Decapentaplegic protein precursor (DPP-C protein).
 GN DPP.
 OS Drosophila simulans (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 CX NCBI_Taxid=7240;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NET DPL;
 RX MEDLINE=97225212; PubMed=9071585;
 RA Newfield S.J., Padgett R.W., Findley S.D., Richter B.G., Sanicola M.,
 RA de Cuevas M., Gelbart W.M.;
 RT "Molecular evolution at the decapentaplegic locus in Drosophila";
 RL Genetics 145:297-309(1997).

CC -1- FUNCTION: ACTS AS AN EXTRACELLULAR MORPHOGEN TO ESTABLISH AT LEAST
 CC TWO CELLULAR RESPONSE THRESHOLDS WITHIN THE DORSAL HALF OF THE
 CC DROSOPHILA EMBRYO. REQUIRED FOR THE PROPER DEVELOPMENT OF THE
 CC EMBRYONIC DORSAL HYPODERM, FOR VIABILITY OF LARVAE AND FOR CELL
 CC VIABILITY OF THE EPITHELIAL CELLS IN THE IMAGINAL DISKS. ACTS
 CC TOGETHER WITH SCW (BY SIMILARITY).
 CC -1- SUBUNIT: HETERODIMERS OF SCW/DPP ARE THE ACTIVE SUBUNIT, DPP/DPP
 CC HOMODIMERS ELICIT A BASAL RESPONSE AND SCW/SCW HOMODIMERS ALONE
 CC ARE INEFFECTIVE IN SPECIFYING A DORSAL PATTERN (BY SIMILARITY).
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN THE IMAGINAL DISCS ASSOCIATED

CC WITH ESTABLISHMENT OF THE PROXIMAL-DISTAL AXIS OF THE APPENDAGES,
 CC AND MIDGUT MESODERM (BY SIMILARITY).
 CC -1- SIMILARITY: Belongs to the TGF-beta family.
 CC -----
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CC EMBL; U63854; AAC47554.1; -.
 DR HSPF; P12643; 3BMP.
 DR FlyBase; FBgn0015673; Dsrm\pdp.
 DR InterPro; IPR001839; TGFb.
 DR InterPro; IPR001111; TGFb.N.
 DR Pfam; PF000019; TGF-beta; 1.
 DR Pfam; PF00688; TGFb_propeptide; 1.
 DR ProDom; PD000357; TGFb; 1.
 DR SMART; SM00204; TGFb; 1.
 DR SMART; SM00250; TGF_BETA_1; 1.
 DR Growth factor; Developmental protein; Differentiation; Glycoprotein;
 KW SIGNAL.
 FT PROPEP 1 15
 FT CHAIN 16 461
 FT DISULFID 462 593
 FT DISULFID 492 558
 FT DISULFID 521 590
 FT DISULFID 525 592
 FT DISULFID 557 557
 FT CARBOHYD 122 122
 FT CARBOHYD 347 347
 FT CARBOHYD 382 382
 FT CARBOHYD 534 534
 SQ SEQUENCE 593 AA; 66248 MW; F0BDB21209F44380 CRC64;

Query Match 53.5%; Score 347; DB 1; Length 593;
 Best Local Similarity 49.6%; Pred. No. 1.4e-29;
 Matches 58; Conservative 24; Mismatches 33; Indels 2; Gaps 1;

QY 5 RQGRPS--KNLKRCSRKALHVFKDMGMDWMTIAPLEAEFHCGLCEPPLRSHLEPT 62
 DB 477 RQPRRPTRRKNDHDTCRHSLYVDFSDVGNDWVAIPGQAFYCHDCCFPLADHNS 536
 QY 63 NEAVITQTMNSMDEPSTPPACVPTLSPISIFISANNVYKQVEDMVESGCGR 119
 DB 537 NEAVITQTMNSMDEPSTPPACVPTLSPISIFISANNVYKQVEDMVESGCGR 553

RESULT 15
 ID BMP4_CHICK STANDARD; PRT; 405 AA.
 AC Q90752;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Bone morphogenetic protein 4 precursor (BMP-4).
 GN BMP4 OR BMP-4.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 CX NCBI_Taxid=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=White leghorn;
 RX MEDLINE=94163974; PubMed=8119128;
 RA Francis P.H., Richardson M.K., Brickell P.M., Tickle C.;
 RT "Bone morphogenetic proteins and a signalling pathway that controls
 RT patterning in the developing chick limb";
 RL Development 120:209-218(1994).
 RN [2]

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OM protein - protein search, using sw model

Run on: February 18, 2004, 17:39:10 ; Search time 35 Seconds

(without alignments)
877.379 Million cell updates/sec

Title: US-09-701-121-2

Perfect score: 649

Sequence: 1 PLATQGRPSKNLKARCSR.....ANNVYKQYEDMWVESGCR 119

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

1: SP_archaea:*
2: SP_bacteria:*
3: SP_fungi:*
4: SP_human:*
5: SP_invertebrate:*
6: SP_mammal:*
7: SP_mhc:*
8: SP_organelle:*
9: SP_phage:*
10: SP_plant:*
11: SP_rodent:*
12: SP_virus:*
13: SP_vertebrate:*
14: SP_unclassified:*
15: SP_virus:*
16: SP_bacteriaph:*
17: SP_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB ID | Description |
|------------|-------|---------------|--------|-------|---------------------|
| 1 | 640 | 98.6 | 249 | 11 | Q8BRW9 mus musculus |
| 2 | 637 | 98.2 | 500 | 13 | Q9W6G0 gallus galli |
| 3 | 587 | 90.4 | 324 | 13 | Q9YHW9 gallus galli |
| 4 | 563 | 86.7 | 257 | 13 | Q42303 brachydanio |
| 5 | 534.5 | 82.4 | 126 | 13 | Q93573 gallus galli |
| 6 | 527.5 | 81.3 | 261 | 13 | Q9W6C0 brachydanio |
| 7 | 527 | 81.2 | 413 | 13 | Q9DGN4 xenopus lae |
| 8 | 524 | 80.7 | 399 | 13 | Q9W753 xenopus lae |
| 9 | 524 | 80.7 | 412 | 13 | Q12938 brachydanio |
| 10 | 491 | 75.7 | 294 | 6 | Q8BDW9 macaca fasc |
| 11 | 491 | 75.7 | 447 | 6 | Q9BDM6 cercopithec |
| 12 | 386 | 59.5 | 441 | 11 | Q99MY1 mus musculu |
| 13 | 368.5 | 56.8 | 361 | 5 | Q96504 branchiosto |
| 14 | 368 | 56.7 | 204 | 5 | Q9XZ69 tripeustes |
| 15 | 366 | 56.4 | 411 | 5 | Q9U418 branchiosto |
| 16 | 365 | 56.2 | 405 | 5 | Q9U588 ptychodera |

| | | | | | |
|----|-------|------|-----|----|---------------------|
| 17 | 361 | 55.6 | 289 | 5 | Q9XY08 strongyloce |
| 18 | 359 | 55.3 | 417 | 5 | Q9XY07 lycechinus |
| 19 | 357.5 | 55.1 | 509 | 5 | Q8WS99 archaster l |
| 20 | 357 | 55.0 | 67 | 11 | Q8K4X5 rattus norv |
| 21 | 355.5 | 54.8 | 178 | 5 | Q25211 junonia coe |
| 22 | 355.5 | 54.8 | 461 | 5 | Q8WX23 hemicentrot |
| 23 | 354 | 54.5 | 67 | 6 | Q02783 bos taurus |
| 24 | 350 | 53.9 | 277 | 13 | Q90Y82 lampetia ja |
| 25 | 349.5 | 53.9 | 411 | 13 | Q9369 brachydanio |
| 26 | 349.5 | 53.9 | 411 | 13 | Q9369 brachydanio |
| 27 | 348 | 53.6 | 398 | 13 | Q90YD7 xenopus tro |
| 28 | 347.5 | 53.5 | 128 | 5 | Q95W38 stictocerc |
| 29 | 347 | 53.5 | 588 | 5 | Q9YOC6 acropora m |
| 30 | 346 | 53.3 | 400 | 13 | Q73818 xenopus lae |
| 31 | 346 | 53.3 | 400 | 13 | Q91703 xenopus lae |
| 32 | 346 | 53.3 | 443 | 5 | Q76851 halocynthia |
| 33 | 345 | 53.2 | 400 | 13 | Q90YD6 brachydanio |
| 34 | 344.5 | 53.1 | 411 | 13 | Q13108 schistocerc |
| 35 | 343 | 52.9 | 378 | 5 | Q8MXC2 acropora m |
| 36 | 342.5 | 52.8 | 191 | 5 | Q26468 schistocerc |
| 37 | 342 | 52.7 | 373 | 13 | Q98950 gallus galli |
| 38 | 342 | 52.7 | 373 | 13 | Q90723 gallus galli |
| 39 | 342 | 52.7 | 400 | 13 | Q57574 brachydanio |
| 40 | 342 | 52.7 | 407 | 5 | Q8MWG4 patella vul |
| 41 | 341 | 52.5 | 422 | 5 | Q8IAE3 stichopus j |
| 42 | 340 | 52.4 | 400 | 13 | Q13107 brachydanio |
| 43 | 340 | 52.4 | 403 | 13 | Q8JIK0 cyrtichrom |
| 44 | 340 | 52.4 | 403 | 13 | Q8J177 julidochrom |
| 45 | 340 | 52.4 | 403 | 13 | Q8J1J4 steatocranu |

ALIGNMENTS

RESULT 1

Q8BRW9 PRELIMINARY; PRT; 249 AA.
ID Q8BRW9
AC Q8BRW9
DT 01-MAR-2003 (TREMblrel. 23, Created)
DI 01-MAR-2003 (TREMblrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)
DE Growth differentiation factor 5 (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Aorta and vein;
RX MEDLINE=22354683; PubMed=1246851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.
RL Nature 420:563-573 (2002).
DR EMBL; AK041168; BAC30847.1; -
FT NON TER
SQ SEQUENCE 249 AA; 28409 MW; EGEA047F06B57189 CRC64;

Query Match Best Local Similarity 98.6%; Score 640; DB 11; Length 249;
Matches 117; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 PLATQGRPSKNLKARCSRKALVHVKDMGWDWMTIAPLEYEFHGEHCCEPLRSHLE 60
Db 131 PLATQGRPSKNLKARCSRKALVHVKDMGWDWMTIAPLEYEFHGEHCCEPLRSHLE 190
QY 61 PTNHAVIQTLMSNDPESTPPTACVPTPLSPISILFDSANNVYKQYEDMWVESGCR 119
Db 191 PTNHAVIQTLMSNDPESTPPTCCVPTPLSPISILFDSANNVYKQYEDMWVESGCR 249

RESULT 2

Q9W6G0 ID Q9W6G0 PRELIMINARY; PRT; 500 AA.

AC Q9W6G0; 01-NOV-1999 (TrEMBLrel. 12, Created)

DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)

DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

DE GDF-5 protein.

GN GDF5.

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

OC NCBI_TaxID=9031; 1]

OX NCBI_TaxID=9031; 1]

RP SEQUENCE FROM N.A.

RX MEDLINE=99146893; PubMed=10021348; Francis-West P.H., Abdelfattah A., Chen P., Allen C., Parish J., Lader R., Allen S., Macpherson S., Luyten F.P., Archer C.W.; "Mechanisms of GDF-5 action during skeletal development.";

RT Development 126:1305-1315(1999).

RL -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.

CC EMBL; AF123389; AAD30451.1; -.

DR HSSP; P12643; 3BMP.

DR InterPro; IPR002400; GF_cysknot.

DR InterPro; IPR002405; Inhibin_alpha.

DR InterPro; IPR001839; TGFb.

DR InterPro; IPR001111; TGFb_N.

DR Pfam; PF00019; TGF-beta_1.

DR Pfam; PF00688; TGFb_propeptide; 1.

DR PRINTS; PR00438; GFCYSKNOT.

DR PRINTS; PR00669; INHIBINA.

DR PRODOM; PD000357; TGFb; 1.

DR SMART; SM00204; TGFb; 1.

DR PROSITE; PS00250; TGF_BETA_1; 1.

SO SEQUENCE 500 AA; 55952 MW; 1DE8395A3119A598 CRC64;

Query Match 98.2%; Score 637; DB 13; Length 500; Best Local Similarity 97.5%; Pred. No. 8.6e-67; Matches 116; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 PLATROGKRPSSKNLKARCSKRALHVNFKMGMDWMTAPLEYEAFHCEGCEPFLRSHLE 60

DB 382 PLATROGKRPSSKNLKARCSKRALHVNFKMGMDWMTAPLEYEAFHCEGCEPFLRSHLE 441

QY 61 PTNNAVIQTLNMSMDPESTPTPTACVPRTRSPISILFTDSANNVYKQYED 119

DB 442 PTNNAVIQTLNMSMDPESTPTPTCCVPTRLSPISILFTDSANNVYKQYEDMVVESCGR 500

RESULT 3

Q9YHW9 ID Q9YHW9 PRELIMINARY; PRT; 324 AA.

AC Q9YHW9; 01-MAY-1999 (TrEMBLrel. 10, Created)

DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)

DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)

DE Growth differentiation factor 5 (Fragment).

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

OC NCBI_TaxID=9031; 1]

OX NCBI_TaxID=9031; 1]

RP SEQUENCE FROM N.A.

RX MEDLINE=99119366; PubMed=9918693; Merino R., Macias D., Ganan Y., Economides A.N., Wang X., Wu Q., Stahl N., Sampath K.T., Varona P., Hurlie J.M.; "Expression and function of Gdf-5 during digit skeletogenesis in the embryonic chick leg bud.";

RT Dev. Biol. 206:33-45(1999).

CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.

EMBL; AF075441; AAD14568.1; -.

DR HSSP; P12643; 3BMP.

DR InterPro; IPR002405; Inhibin_alpha.

DR InterPro; IPR001839; TGFb_N.

DR InterPro; IPR001111; TGFb_N.

DR Pfam; PF00019; TGF-beta; 1.

DR Pfam; PF00688; TGFb_propeptide; 1.

DR PRINTS; PR00669; INHIBINA.

DR PRODOM; PD000357; TGFb; 1.

DR SMART; SM00204; TGFb; 1.

DR PROSITE; PS00250; TGF_BETA_1; 1.

FT NON TER 1 1

FT NON TER 1 1

SO SEQUENCE 324 AA; 37206 MW; 0B847CB11375007 CRC64;

Query Match 90.4%; Score 587; DB 13; Length 324; Best Local Similarity 97.3%; Pred. No. 4.3e-61; Matches 107; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLATROGKRPSSKNLKARCSKRALHVNFKMGMDWMTAPLEYEAFHCEGCEPFLRSHLE 60

DB 215 PLATROGKRPSSKNLKARCSKRALHVNFKMGMDWMTAPLEYEAFHCEGCEPFLRSHLE 274

QY 61 PTNNAVIQTLNMSMDPESTPTPTACVPRTRSPISILFTDSANNVYKQYED 110

DB 275 PTNNAVIQTLNMSMDPESTPTPTCCVPTRLSPISILFTDSANNVYKQYED 324

RESULT 4

Q42303 ID Q42303 PRELIMINARY; PRT; 257 AA.

AC Q42303; 01-JAN-1998 (TrEMBLrel. 05, Created)

DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)

DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

DE Contact (Fragment).

GN GDF5.

OS Brachydanio rerio (Zebrafish) (Danio rerio).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.

OC NCBI_TaxID=7955; 1]

OX NCBI_TaxID=7955; 1]

RP SEQUENCE FROM N.A.

RX MEDLINE=97398455; PubMed=9256353; Bruneau S., Mourrain P., Rosa F.M.; "Expression of contact, a new zebrafish DVR member, marks mesenchymal cell lineages in the developing pectoral fins and head and is regulated by retinoic acid.";

RT Mech. Dev. 65:163-173(1997).

CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.

EMBL; Y12005; CAA72733.1; -.

DR HSSP; P12643; 3BMP.

DR ZFIN; ZDB-GENE-990415-39; gdf5.

DR InterPro; IPR002400; GF_cysknot.

DR InterPro; IPR002405; Inhibin_alpha.

DR InterPro; IPR001839; TGFb.

DR Pfam; PF00019; TGF-beta; 1.

DR PRINTS; PR00438; GFCYSKNOT.

DR PRINTS; PR00669; INHIBINA.

DR PRODOM; PD000357; TGFb; 1.

DR SMART; SM00204; TGFb; 1.

DR PROSITE; PS00250; TGF_BETA_1; 1.

FT NON TER 1 1

FT NON TER 1 1

SO SEQUENCE 257 AA; 29787 MW; 6D64F05422948849 CRC64;

Query Match 86.7%; Score 563; DB 13; Length 257; Best Local Similarity 86.0%; Pred. No. 2.3e-58; Matches 98; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

QY 6 OKRRSSKNLKARCSKRALHVNFKMGMDWMTAPLEYEAFHCEGCEPFLRSHLEPTNNA 65

DB 144 OKRRSSKNLKARCSKRALHVNFKMGMDWMTAPLEYEAFHCEGCEPFLRSHLEPTNNA 203

QY 66 VIOTLMSNDPESTPTACVPTRLSPISILFTDSANNVYKQYEDMVVSCGCR 119
 Db 204 IOTLMSNDPESTPTCCVPTRLSPISILYIDSANNVYKQYEDMVVSCGCR 257

RESULT 5

093573 PRELIMINARY; PRT; 126 AA.
 AC 093573;
 DT 01-NOV-1998 (TREMBlrel. 08, Created)
 DT 01-NOV-1998 (TREMBlrel. 08, last sequence update)
 DT 01-OCT-2002 (TREMBlrel. 22, last annotation update)
 DE Putative growth/differentiation factor 6/7 (Fragment).
 GN GDF6/7.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99026113; PubMed=9808626;
 RA Lee K.-J., Mendelsohn M., Jessell T.M.;
 RT "Neuronal patterning by BMPs: a requirement for GDF7 in the generation
 of a discrete class of commissural interneurons in the mouse spinal
 cord".
 RL Genes Dev. 12:3394-3407(1998).
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
 DR EMBL; AF089086; AAC97113.1; -.
 DR HSSP; P12643; 3BMP.
 DR InterPro; IPR002400; GF_cyskn0t.
 DR InterPro; IPR001839; TGFb.
 DR InterPro; IPR001839; TGFb.
 DR Pfam; PF00019; TGF-beta; 1.
 DR PRINTS; PR00438; GFCYSKN0T.
 DR PRINTS; PR00669; INHIBIN.
 DR ProDom; PD000357; TGFb; 1.
 DR SMART; SM00204; TGFb; 1.
 DR PROSITE; PS00250; TGF_BETA_1; 1.
 FT NON TER 1
 SQ SEQUENCE 126 AA; 14265 MW; CB824D280F44A394 CRC64;

Query Match 82.4%; Score 534.5; DB 13; Length 126;
 Best Local Similarity 79.0%; Pred. No. 2.4e-55;
 Matches 94; Conservative 13; Mismatches 11; Indels 1; Gaps 1;
 QY 2 LATROGKR-PSKXNKAROSRKALHVNFKMGMDMTAPLEYEAHCEGLCEPLRSHTL 60
 Db 8 IAASSGGRGHGKAKKTKSRKPLHVNFKELGMDMTAPLDYEAHCEGVCDPLRSHTL 67
 QY 61 PTNHAIVQTLMSNDPESTPTACVPTRLSPISILFTDSANNVYKQYEDMVVSCGCR 119
 Db 68 PTNHAIVQTLMSNDPESTPTSCVPSKLSPLISILYIDSANNVYKQYEDMVVETCCGR 126

RESULT 6

09W6CO PRELIMINARY; PRT; 261 AA.
 AC 09W6CO;
 DT 01-NOV-1999 (TREMBlrel. 12, Created)
 DT 01-NOV-1999 (TREMBlrel. 12, last sequence update)
 DT 01-OCT-2002 (TREMBlrel. 22, last annotation update)
 DE Growth/differentiation factor 7 (Fragment).
 GN GPF7.
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99148135; PubMed=10022976;

RA Davidson A.J., Postlethwait J.H., Yan Y.L., Beier D.R., van Doren C.,
 RA Fournzier D., Celeste A.J., Crosier K.E., Crosier P.S.;
 RT "Isolation of zebrafish gdf7 and comparative genetic mapping of genes
 belonging to the Growth/Differentiation factor 5, 6, 7 subgroup of the
 RT TGF-beta superfamily.";
 RL Genome Res. 9:121-129(1999).
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
 DR EMBL; AF113023; AAD08829.1; -.
 DR HSSP; P12643; 3BMP.
 DR ZFIN; ZDB-GENE-990714-1; gdf7.
 DR InterPro; IPR002400; GF_cyskn0t.
 DR InterPro; IPR002405; Inhibin_alpha.
 DR InterPro; IPR001839; TGFb.
 DR Pfam; PF00019; TGF-beta; 1.
 DR PRINTS; PR00438; GFCYSKN0T.
 DR PRINTS; PR00669; INHIBIN.
 DR ProDom; PD000357; TGFb; 1.
 DR SMART; SM00204; TGFb; 1.
 DR PROSITE; PS00250; TGF_BETA_1; 1.
 FT NON TER 1
 SQ SEQUENCE 261 AA; 29414 MW; 77346E977036A104 CRC64;

Query Match 81.3%; Score 527.5; DB 13; Length 261;
 Best Local Similarity 76.0%; Pred. No. 3.7e-54;
 Matches 95; Conservative 11; Mismatches 12; Indels 7; Gaps 1;
 QY 2 LATROGKR-----SKXNKAROSRKALHVNFKMGMDMTAPLEYEAHCEGLCEPL 54
 Db 137 LAGRPVGPPLTSGGKGGRRRTSRKPLHVNFKELGMDMTAPLDYEAHCEGLCDFP 196
 QY 55 LRSHLEPTNHAIVQTLMSNDPESTPTACVPTRLSPISILFTDSANNVYKQYEDMVVE 114
 Db 197 LRSHLEPTNHAIVQTLMSNDPESTPTSCVPSKLSPLISILYIDSANNVYKQYEDMVVE 256

QY 115 SCGCR 119
 Db 257 SCGCR 261

RESULT 7

09DGN4 PRELIMINARY; PRT; 413 AA.
 AC 09DGN4;
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, last annotation update)
 DE Growth/differentiation factor 16 precursor protein.
 GN GPF16.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20368184; PubMed=10906478;
 RA Vokes S.A., Krieg P.A.;
 RT "Gdf16, a novel member of the growth/differentiation factor subgroup
 of the TGF-beta superfamily, is expressed in the hindbrain and
 RT epibranchial placodes.";
 RL Mech. Dev. 95:279-282(2000).
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
 DR EMBL; AF239676; AAF99597.1; -.
 DR HSSP; P12643; 3BMP.
 DR InterPro; IPR002400; GF_cyskn0t.
 DR InterPro; IPR001839; TGFb.
 DR InterPro; IPR001111; TGFb_N.
 DR Pfam; PF00019; TGF-beta; 1.
 DR Pfam; PR00688; TGFb_propeptide; 1.
 DR PRINTS; PR00438; GFCYSKN0T.
 DR ProDom; PD000357; TGFb; 1.
 DR SMART; SM00204; TGFb; 1.
 DR PROSITE; PS00250; TGF_BETA_1; 1.

```

KW Signal.
FT SIGNAL.
SQ SEQUENCE 1 23 POTENTIAL.
413 AA; 46510 MW; 5F1B0D7D97E591F6 CRC64;

Query Match
Best Local Similarity 77.3%; Pred. No. 7, 3e-54;
Matches 92; Conservative 13; Mismatches 14; Indels 0; Gaps 0;

QY 1 PLATOGKRRPSKILKARCSRKALHVNFKDMGMDWIIAPLEYEAFHCEGLCEPLRSHLE 60
DB 295 PRTNNGKHAKSKSRCSKPLVNFKEIGMDWIIAPLEYEAFHCEGLCEPLRSHLE 354
QY 61 PTHNAVITLMSMDEPSTPPACVPTLSPISILFISANNVVKQYEDMVVSCGCR 119
DB 355 PTHNAVITLMSMDEPSTPPSCVPSKLSPIISILYIDSGNNVVKQYEDMVVSCGCR 413

RESULT 8
Q9W753 PRELIMINARY; PRT; 399 AA.
ID 09W753
AC 09W753
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Growth and differentiation factor 6.
GN GDF6.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus.
OC NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9936700; PubMed=10393114;
RA Chang C., Hemmati-Bityanlou A.;
RT "Xenopus GDF6, a new antagonist of noggin and a partner of BMPs.";
RL Development 126:3347-3357(1999).
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR EMBL; AF155125; AAD38402.1; -.
DR HSSP; P12643; 3BMP.
DR InterPro; IPR002400; GF_cysknob.
DR InterPro; IPR002405; Inhibin_alpha.
DR InterPro; IPR001839; TGFb.
DR InterPro; IPR001111; TGFb N.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGF-propeptide; 1.
DR PRINTS; PR00438; GFCYSKNOT.
DR PRODOM; PD000357; TGFb N.
DR SMART; SM00204; TGFb; 1.
DR PROSITE; PS00250; TGF_BETA_1; 1.
SQ SEQUENCE 399 AA; 45571 MW; C549D973B50B8517 CRC64;

Query Match
Best Local Similarity 77.6%; Score 524; DB 13; Length 399;
Matches 90; Conservative 15; Mismatches 11; Indels 0; Gaps 0;

QY 4 TRQGKRPSSKILKARCSRKALHVNFKDMGMDWIIAPLEYEAFHCEGLCEPLRSHLEPTN 63
DB 284 SRGKHGRKSRKSKPLVNFKEIGMDWIIAPLEYEAFHCEGLCEPLRSHLEPTN 343
QY 64 HAVIQTLMNSMDEPSTPPACVPTLSPISILFISANNVVKQYEDMVVSCGCR 119
DB 344 HAVIQTLMNSMDEPSTPPSCVPSKLSPIISILYIDSGNNVVKQYEDMVVSCGCR 399

RESULT 9
ID 012938 PRELIMINARY; PRT; 412 AA.
AC 012938
DT 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)

```

```

DE Dynamo protein precursor.
GN GDF6 OR DYNAMO.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes;
OC Cyprinidae; Danio.
OC NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Embryo;
RA MEDLINE=97231294; PubMed=9076689;
RA Bruneau S., Rosa F.;
RT "Dynamo a new zebrafish DVR member of the TGF-B superfamily is
RT expressed in the posterior neural tube and is up regulated by sonic
RT hedgehog.";
RL Mech. Dev. 61:199-212(1997).
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR EMBL; X99769; CAA68102.1; -.
DR HSSP; P12643; 3BMP.
DR ZFIN; ZDB-GENE-980526-442; gdf6a.
DR InterPro; IPR002400; GF_cysknob.
DR InterPro; IPR002405; Inhibin_alpha.
DR InterPro; IPR001839; TGFb.
DR InterPro; IPR001111; TGFb N.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGF-propeptide; 1.
DR PRINTS; PR00438; GFCYSKNOT.
DR PRODOM; PD000357; TGFb N.
DR SMART; SM00204; TGFb; 1.
DR PROSITE; PS00250; TGF_BETA_1; 1.
KM SIGNAL.
FT CHAIN 1 17 POTENTIAL.
FT SIGNAL 293 412 DYNAMO PROTEIN.
SQ SEQUENCE 412 AA; 47072 MW; 4076E262C4481121 CRC64;

Query Match
Best Local Similarity 80.7%; Score 524; DB 13; Length 412;
Matches 88; Conservative 18; Mismatches 12; Indels 0; Gaps 0;

QY 2 LATOGKRRPSKILKARCSRKALHVNFKDMGMDWIIAPLEYEAFHCEGLCEPLRSHLEPTN 61
DB 295 LPRHGRKSRKSKSKPLVNFKEIGMDWIIAPLEYEAFHCEGLCEPLRSHLEPTN 354
QY 62 HAVIQTLMNSMDEPSTPPACVPTLSPISILFISANNVVKQYEDMVVSCGCR 119
DB 355 HAVIQTLMNSMDEPSTPPSCVPSKLSPIISILYIDSGNNVVKQYEDMVVSCGCR 412

RESULT 10
Q9BDW9 PRELIMINARY; PRT; 294 AA.
ID 09BDW9
AC 09BDW9
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Growth/differentiation factor 7 (Fragment).
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OC NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Cerebral cortex motor area;
RX MEDLINE=21136583; PubMed=11238730;
RA Watake A., Fujita H., Hayashi M., Yamamoto T.;
RT "Growth/differentiation factor 7 is preferentially expressed in the
RT primary motor area of the monkey neocortex.";
RL J. Neurochem. 76:1455-1464(2001).
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR EMBL; AF254567; AAK27794.1; -.
DR HSSP; P12643; 3BMP.

```


DR InterPro: IPR001111; TGFb N.
DR Pfam: PF00688; TGFb_propeptide; 1.
DR PRINTS: PR00669; INHIBINA.
DR ProDom: PD000357; TGFb; 1.
DR SMART: SM00204; TGFb; 1.
DR PROSITE: PS00250; TGF_BETA_1; 1.
SQ SEQUENCE 361 AA; 41517 MW; 09FF5FE6C9785DD1 CRC64;

Query Match 56.8%; Score 368.5; DB 5; Length 361;
Best Local Similarity 52.0%; Pred. No. 3.6e-35;
Matches 64; Conservative 25; Mismatches 23; Indels 5; Gaps 1;

QY 2 IATRO-----GKPSKNTLKARCSKALHVNFKDMGMDWIIAPLEYEAFHCEGLCEPPIR 56
DB 239 VASRQKRAKGRKKORRRKLCANCRHSLYDFSDVGMDWIVAPGQAYYCHGECFPPLA 298
DB 299 DHINSTNIAIVQTLVNSVNPALVPKACCVPTDLSPTSMKLYINENDQVVLKNYQDMVVEGCG 358
QY 117 GCR 119
DB 359 GCR 361

RESULT 14

Q9XZ69 PRELIMINARY; PRT; 204 AA.
AC Q9XZ69;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Bone morphogenetic protein 2/4 homolog (Fragment).
GN BMP2/4.
OS Tripneustes gratilla (Hawaiian sea urchin).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinoidae; Euechinoidae; Echinacea; Temnopleuroidea; Toxopneustidae;
OC Tripneustes.
OX NCBI_TaxID=7673;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99262121; PubMed=10329409;
RA Hwang S.L., Chen C.A., Chen C.;
RT "Sea urchin TgBMP2/4 gene encoding a bone morphogenetic protein
RT closely related to vertebrate BMP2 and BMP4 with maximal expression at
RT the later stages of embryonic development.";
RL Biochem. Biophys. Res. Commun. 258:457-463 (1999).
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR EMBL: AF133305; AAD30538.1; -.
DR HSSP: P12643; 3BMP.
DR InterPro: IPR002400; GF_cysknct.
DR InterPro: IPR002405; Inhibin_alpha.
DR InterPro: IPR001839; TGFb.
DR InterPro: IPR001111; TGFb N.
DR Pfam: PF00019; TGF-beta; 1.
DR PRINTS: PR00688; TGFb_propeptide; 1.
DR PRINTS: PR00669; INHIBINA.
DR ProDom: PD000357; TGFb; 1.
DR SMART: SM00204; TGFb; 1.
DR PROSITE: PS00250; TGF_BETA_1; 1.
FT NON TER 1
SQ SEQUENCE 204 AA; 23697 MW; CE829BDC2AA9F077 CRC64;

Query Match 56.7%; Score 368; DB 5; Length 204;
Best Local Similarity 53.8%; Pred. No. 2.2e-35;
Matches 63; Conservative 19; Mismatches 35; Indels 0; Gaps 0;

QY 3 ATGQKRPSSKNTLKARCSKALHVNFKDMGMDWIIAPLEYEAFHCEGLCEPPIRSHLEPT 62
DB 88 SSKSRKRRKGRRLKANCRRHSLYDFSDVGMDWIVAPGQAYYCHGECFPPLAEHLNNTT 147

QY 63 NHAIVQTLNMSMDPESTPTACVPTPLSPISLIFIDSANNVYKQYEDMVVSGGCR 119
DB 148 NHAIVQTLVNSVNPALVPKACCVPTDLSPTSMKLYINENDQVVLKNYQDMVVEGCGCR 204

RESULT 15

Q9U418 PRELIMINARY; PRT; 411 AA.
AC Q9U418;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Bone morphogenetic protein 2/4.
GN BMP2/4.
OS Branchiostoma belcheri (Amphioxus).
OC Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
OC Branchiostoma.
OX NCBI_TaxID=7741;
RN [1]
RP SEQUENCE FROM N.A.
RA Yasui K., Saiga H., Temura M., Semba I.;
RT "Early body formation and expression pattern of genes encoding
RT secreted proteins, BbBMP2/4, BbWnt7, and BbWnt8 in lancelets.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR EMBL: AF206325; AAF19841.1; -.
DR HSSP: P12643; 3BMP.
DR InterPro: IPR002405; Inhibin_alpha.
DR InterPro: IPR001839; TGFb.
DR InterPro: IPR001111; TGFb N.
DR Pfam: PF00019; TGF-beta; 1.
DR Pfam: PF00688; TGFb_propeptide; 1.
DR PRINTS: PR00669; INHIBINA.
DR ProDom: PD000357; TGFb; 1.
DR SMART: SM00204; TGFb; 1.
DR PROSITE: PS00250; TGF_BETA_1; 1.
SQ SEQUENCE 411 AA; 46929 MW; F579898060F18355 CRC64;

Query Match 56.4%; Score 366; DB 5; Length 411;
Best Local Similarity 53.0%; Pred. No. 8.3e-35;
Matches 62; Conservative 23; Mismatches 32; Indels 0; Gaps 0;

QY 3 ATGQKRPSSKNTLKARCSKALHVNFKDMGMDWIIAPLEYEAFHCEGLCEPPIRSHLEPT 62
DB 295 ANGRKKHGRRLKANCRRHSLYDFSDVGMDWIVAPGQAYYCHGECFPPLADHLNST 354
QY 63 NHAIVQTLNMSMDPESTPTACVPTPLSPISLIFIDSANNVYKQYEDMVVSGGCR 119
DB 355 NHAIVQTLVNSVNPALVPKACCVPTDLSPTSMKLYINENDQVVLKNYQDMVVEGCGCR 411

Search completed: February 18, 2004, 17:43:20
Job time : 36 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 18, 2004, 17:36:44 ; Search time 40 Seconds

(without alignments)
472.212 Million cell updates/sec

Title: US-09-701-121-2

Sequence: 1 PLATROGKRPKNLARCGR.....ANNVYKQYEDWVESGCR 119

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1 | 649 | 100.0 | 119 | 21 | AA44296 |
| 2 | 645 | 99.4 | 119 | 17 | AAW06920 |
| 3 | 645 | 99.4 | 119 | 18 | AAW19846 |
| 4 | 645 | 99.4 | 120 | 16 | AAW78731 |
| 5 | 645 | 99.4 | 120 | 18 | AAW26590 |
| 6 | 645 | 99.4 | 120 | 22 | AAW10973 |
| 7 | 645 | 99.4 | 120 | 24 | ABG73290 |
| 8 | 645 | 99.4 | 401 | 14 | AAW40800 |
| 9 | 645 | 99.4 | 501 | 16 | AAW69600 |

| | | | | | | |
|----|-----|------|-----|----|----------|--------------------|
| 10 | 645 | 99.4 | 501 | 18 | AAW36100 | Human MP52. Homo |
| 11 | 645 | 99.4 | 501 | 18 | AAW19210 | Human TGF-beta pro |
| 12 | 645 | 99.4 | 501 | 18 | AAW11900 | Human high mol. wt |
| 13 | 645 | 99.4 | 501 | 18 | AAW01799 | Human MP52 protein |
| 14 | 645 | 99.4 | 501 | 18 | AAW12770 | Human bone morphog |
| 15 | 645 | 99.4 | 501 | 19 | AAW44868 | TGF-beta superfam |
| 16 | 645 | 99.4 | 501 | 19 | AAW33008 | Human MP52. Homo |
| 17 | 645 | 99.4 | 501 | 22 | AAW70529 | Human TGF-beta MP5 |
| 18 | 640 | 98.6 | 495 | 15 | AAW60022 | Growth differentia |
| 19 | 640 | 98.6 | 495 | 22 | AAW84550 | Amino acid sequenc |
| 20 | 640 | 98.6 | 495 | 24 | ABG76018 | Wild type mature h |
| 21 | 639 | 98.5 | 119 | 21 | AAW70752 | Methionine oxidase |
| 22 | 639 | 98.5 | 119 | 21 | AAW70756 | Trypophan alanyl |
| 23 | 639 | 98.5 | 119 | 21 | AAW70757 | Human TGFbeta prot |
| 24 | 639 | 98.5 | 119 | 21 | AAW70758 | Cartilage-derived |
| 25 | 639 | 98.5 | 120 | 23 | AAW51932 | Human CDMP-1/GDF-5 |
| 26 | 639 | 98.5 | 501 | 17 | AAW95635 | Human CDMP-1/GDF-5 |
| 27 | 639 | 98.5 | 501 | 21 | AAW92034 | Human CDMP-1/GDF-5 |
| 28 | 559 | 86.1 | 102 | 21 | AAW09553 | Human TGFbeta pro |
| 29 | 559 | 86.1 | 102 | 21 | AAW02819 | Human CDMP-1/GDF-5 |
| 30 | 559 | 86.1 | 102 | 21 | AAW92578 | Human CDMP-1/GDF-5 |
| 31 | 543 | 83.7 | 120 | 23 | AAW51933 | Human CDMP-1/GDF-5 |
| 32 | 543 | 83.7 | 125 | 24 | ABG76037 | Human TGFbeta pro |
| 33 | 543 | 83.7 | 134 | 16 | AAW66867 | GDF-6. Mus sp. A |
| 34 | 543 | 83.7 | 134 | 21 | AAW12986 | Murine growth diff |
| 35 | 543 | 83.7 | 263 | 16 | AAW78739 | Murine growth diff |
| 36 | 543 | 83.7 | 263 | 16 | AAW26595 | Murine BMP-13 homo |
| 37 | 540 | 83.2 | 321 | 18 | AAW78730 | Human mature VL-1 |
| 38 | 540 | 83.2 | 321 | 18 | AAW26591 | Human bone morphog |
| 39 | 540 | 83.2 | 321 | 22 | AAW10982 | Human full length |
| 40 | 540 | 83.2 | 321 | 24 | ABG73298 | Human bone morphog |
| 41 | 540 | 83.2 | 455 | 22 | AAW50216 | Human growth/diffe |
| 42 | 540 | 83.2 | 455 | 23 | AAW79173 | Human growth/diffe |
| 43 | 540 | 83.2 | 455 | 23 | AAW17604 | Human growth/diffe |
| 44 | 538 | 82.9 | 263 | 22 | AAW10985 | Human extracellula |
| 45 | 538 | 82.9 | 263 | 24 | ABG73301 | Murine partial mv2 |

ALIGNMENTS

| | | |
|----------|-------------------------------------------------------------------------|----------------------------------------|
| RESULT 1 | AA44296 | standard; Protein: 119 AA. |
| ID | AA44296 | |
| AC | AA44296 | |
| DT | 29-FEB-2000 | (first entry) |
| XX | XX | |
| DE | Mutant human MP52 monomer protein. | |
| KW | Mutant MP52 monomer protein; transforming growth factor-beta; TGF-beta; | |
| KW | pTGF79 expression vector; osteocyte; bone morphogenetic; osteophtic; | |
| KW | anti-arthritic activity; cartilage; osteoporosis; osteoarthritis; | |
| KW | achondroplasia; fracture; achondroplasia; dyschondrogenesis; | |
| KW | achondrogenesis; palatoschisis; dysosteogenesis. | |
| OS | Homo sapiens. | |
| OS | Synthetic. | |
| FT | Key | Location/Qualifiers |
| FT | Misc-difference 83 | /note= "Wild-type Cys replaced by Ala" |
| XX | XX | |
| PN | MO961611-AL. | |
| XX | XX | |
| PD | 02-DEC-1999. | |
| XX | XX | |
| PF | 14-MAY-1999; | 99WC-1B00866. |
| XX | XX | |
| PR | 22-MAY-1998; | 98WP-0141379. |
| XX | XX | |
| PA | (HMRI) HOECHST MARION ROUSSEL LTD. | |

XX Kawai S, Kimura M, Muraki Y, Katsura M,
 PI WPI; 2000-097122/08.
 DR N-PSDB; AAZ29328.
 XX
 PT Novel monomer protein used for prevention and treatment of bone and/or
 XX cartilage diseases -
 PS Claim 4; Page 20; 26pp; English.
 XX
 CC The present sequence is a mutant human MP52 monomer protein, which
 CC belongs to transforming growth factor-beta (TGF-beta)
 CC superfamily. Mutant MP52 can be produced in E. coli cells by
 CC transforming them with pKOT79 expression vector containing a mutated
 CC MP52 monomer encoding nucleic acid sequence. MP52 monomer protein is
 CC capable of inducing differentiation in osteocytes and exhibits bone
 CC morphogenic, osteoplastic and anti-arthritis activity. The MP52 monomer
 CC protein is used for prevention and treatment of cartilage and/or bone
 CC diseases such as osteoporosis, osteoarthritis, arthrosclerosis, damage of
 CC cartilage, regeneration of bone, cartilage deficit caused by injury and
 CC tumour dissection, fracture, congenital bone and/or cartilage diseases
 CC such as achondroplasia, dyschondrogenesis, achondrogenesis, palatoschisis
 CC and dysosteogenesis and a deficit of root of teeth and a tooth socket.
 SQ Sequence 119 AA;
 Query Match 100.0%; Score 649; DB 21; Length 119;
 Best Local Similarity 100.0%; Pred. No. 6.9e-60;
 Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 PLATROGRRPSKLNKARCSKALHVNFKDGMWDWIIAPLEYAFHCEGICEPILRSHE 60
 Db 1 PLATROGRRPSKLNKARCSKALHVNFKDGMWDWIIAPLEYAFHCEGICEPILRSHE 60
 QY 61 PTNHAVIQTLMNSMDPESTPTACVPTRLSPISILFTDSANNVYKQYEDMVESGCCR 119
 Db 61 PTNHAVIQTLMNSMDPESTPTACVPTRLSPISILFTDSANNVYKQYEDMVESGCCR 119
 RESULT 2
 ID AAM06920 standard; Protein; 119 AA.
 XX
 AC AAM06920;
 XX
 DT 27-JUN-1997 (first entry)
 XX
 DE Human MP52 growth factor residues 383-501.
 XX
 KM Human; MP52; growth factor; monomer; dimer; treatment; bone;
 KM cartilage; dental; disorder; fracture; bone loss;
 KM periodontal disease; calcification; osteoporosis.
 XX
 OS Homo sapiens.
 XX
 PN WO9633215-A1.
 XX
 PD 24-OCT-1996.
 XX
 PF 19-APR-1996; 96WO-JP01062.
 XX
 PR 17-NOV-1995; 95JP-0322403.
 PR 19-APR-1995; 95JP-0093664.
 XX
 PA (FARH) HOECHST JAPAN LTD.
 PI
 PI Ehomoto K, Katsura M, Kawai S, Kimura M, Makishima F;
 PI Matsumoto T, Mikih, Sato Y, Takamatsu H;
 XX WPI: 1996-485730/48.
 DR N-PSDB; AAT46150.
 XX

PT Peptide consisting of part of human MP52 growth factor, and its
 PT dimer - is used for treatment of bone, cartilage and dental
 PT disorders
 XX
 PS Claim 1; Pages 18-19; 33pp; Japanese.
 XX
 CC The present sequence is residues 383 to 501 of the human MP52
 CC growth factor, a dimer of which can be used to treat bone,
 CC cartilage and dental disorders, including fractures, bone loss and
 CC periodontal disease. The dimer was prepared by transforming a host
 CC (preferably E. coli) with a suitable (plasmid) expression vector
 CC containing DNA encoding the monomer. The host was cultured, and
 CC inclusion bodies from the cells worked up to give the monomer,
 CC which was then converted into the dimer. The product was mixed with
 CC type 1 pig tendon collagen and injected into the large thigh vein
 CC of ICR mice. After 20 days 4 of 4 mice injected with 10 microg of
 CC the dimer showed bone/cartilage calcification around the injection
 CC site, compared to none in 0 of 4 mice treated with collagen only.
 SQ Sequence 119 AA;
 Query Match 99.4%; Score 645; DB 17; Length 119;
 Best Local Similarity 99.2%; Pred. No. 1.8e-59;
 Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 PLATROGRRPSKLNKARCSKALHVNFKDGMWDWIIAPLEYAFHCEGICEPILRSHE 60
 Db 1 PLATROGRRPSKLNKARCSKALHVNFKDGMWDWIIAPLEYAFHCEGICEPILRSHE 60
 QY 61 PTNHAVIQTLMNSMDPESTPTACVPTRLSPISILFTDSANNVYKQYEDMVESGCCR 119
 Db 61 PTNHAVIQTLMNSMDPESTPTACVPTRLSPISILFTDSANNVYKQYEDMVESGCCR 119
 RESULT 3
 ID AAM19846 standard; Protein; 119 AA.
 XX
 AC AAM19846;
 XX
 DT 12-FEB-1998 (first entry)
 XX
 DE Human bone inducing factor MP52.
 XX
 KM Human; bone inducing factor; MP52; collagen; fracture;
 KM polyoxyethylene-polyoxypropylene glycol.
 XX
 OS Homo sapiens.
 XX
 PN WO9718829-A1.
 XX
 PD 29-MAY-1997.
 XX
 PF 14-NOV-1996; 96WO-JP03333.
 XX
 PR 17-NOV-1995; 95JP-0322402.
 XX
 PA (FARH) HOECHST JAPAN LTD.
 PI
 PI Shimura T, Toriyama S;
 XX WPI: 1997-310243/28.
 DR N-PSDB; AAT70296.
 XX
 PT Material for repairing bone and collagen, especially bone fracture
 PT or loss - comprising bone-inducing factor and
 PT polyoxyethylene-polyoxypropylene glycol compounds
 XX
 PS Example 4; Page 16-17; 31pp; Japanese.
 CC Bone and collagen inducing material has been developed which comprises
 CC bone inducing factor and polyoxyethylene-polyoxypropylene glycol

CC compound. The present sequence represents human bone inducing factor
 CC MP52. This material allows treatment without surgery. It is highly
 CC absorbable because a carrier is used with the bone inducing factor,
 CC and undergoes reversible sol-gel transition depending on the
 CC temperature.

SQ Sequence 119 AA;

Query Match 99.4%; Score 645; DB 18; Length 119;
 Best Local Similarity 99.2%; Pred. No. 1.8e-59;
 Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLATROGKRPKNLAKRCSRKALHYNFKMGMDWIIAPLEYAHCCEGLCEPPLRSHLE 60
 DB 1 PLATROGKRPKNLAKRCSRKALHYNFKMGMDWIIAPLEYAHCCEGLCEPPLRSHLE 60
 QY 61 PNHAVIQTLMNSMDPESTPTCCVPTRLSPISILFIDSANNVVKQYEDMVEESGCR 119
 DB 61 PNHAVIQTLMNSMDPESTPTCCVPTRLSPISILFIDSANNVVKQYEDMVEESGCR 119

RESULT 4

AAR78731
 ID AAR78731 standard; Protein; 120 AA.

AC AAR78731;
 XX
 DT 25-MAR-2003 (updated)
 DT 23-NOV-1995 (first entry)
 XX
 DE Murine protein MP52.

XX Bone morphogenetic protein; MP52; tendon; ligament.

OS Mus musculus.

XX MO9516035-A2.

XX 15-JUN-1995.

PF 06-DEC-1994; 94WO-US14030.

XX 02-NOV-1994; 94US-0333576.

PR 07-DEC-1993; 93US-0164103.

XX 25-MAR-1994; 94US-0217780.

PA (GENY) GENETICS INST. INC.

PA (HARD) HARVARD COLLEGE.

PI Celeste AJ, Melton DA, Rosen VA, Thomsen GH, Wolfman NM;

PI Wozney JM;

DR WPI: 1995-224320/29.

XX N-PSDB; AAQ96209.

XX Example; Page 51-52; 84pp; English.

CC Oligos #6 and #7 (AAQ96218 & AAQ96219) are used as primers for the
 CC amplification of a 275 bp DNA probe, the internal 269 bp of which
 CC corresp. to nts #607 to #865 of AAQ96207, from the BMP-12 encoding
 CC plasmid subclone PCR1-1#2. This probe was radioactively labelled
 CC and used to screen a murine genomic library. DNA sequence analysis
 CC of one of positively hybridising recombinants named MVR23 indicates
 CC that it encodes a portion of the mouse gene corresp. to the PCR
 CC product mV9 (murine homolog of the MP-52 sequence AAQ96209/R78731).
 CC [Updated on 25-MAR-2003 to correct FN field.]

SQ Sequence 120 AA;

Query Match 99.4%; Score 645; DB 16; Length 120;

Best Local Similarity 99.2%; Pred. No. 1.8e-59;
 Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLATROGKRPKNLAKRCSRKALHYNFKMGMDWIIAPLEYAHCCEGLCEPPLRSHLE 60
 DB 2 PLATROGKRPKNLAKRCSRKALHYNFKMGMDWIIAPLEYAHCCEGLCEPPLRSHLE 61
 QY 61 PNHAVIQTLMNSMDPESTPTCCVPTRLSPISILFIDSANNVVKQYEDMVEESGCR 119
 DB 62 PNHAVIQTLMNSMDPESTPTCCVPTRLSPISILFIDSANNVVKQYEDMVEESGCR 120

RESULT 5

AAW26590
 ID AAW26590 standard; Protein; 120 AA.

XX AAW26590;

AC AAW26590;
 XX
 DT 25-MAR-2003 (updated)
 DT 21-JAN-1998 (first entry)
 XX

DE Human MP52 protein.

XX MP52; BMP; bone morphogenetic protein; human; tendon; ligament;
 XX wound healing; tissue repair; tendonitis; carpal tunnel syndrome;
 XX therapy.

XX Homo sapiens.

FE Key Location/Qualifiers
 FT Protein 1..120
 FT /note= "Claim 5"
 FT Protein 19..120
 FT /note= "Claim 5"

XX US5658882-A.

XX 19-AUG-1997.

PF 22-DEC-1994; 94US-0362670.

XX 22-DEC-1994; 94US-0362670.

PR 07-DEC-1993; 93US-0164103.

XX 25-MAR-1994; 94US-0217780.

PR 02-NOV-1994; 94US-0333576.

PA (GENY) GENETICS INST. INC.

PA (HARD) HARVARD COLLEGE.

PI Celeste AJ, Melton DA, Rosen VA, Thomsen GH, Wolfman NM;

PI Wozney JM;

DR WPI: 1997-424270/39.

XX Claim 5; Column 39-40; 43pp; English.

CC This polypeptide comprises human MP52. A claimed method for
 CC inducing formation of tendon and/or ligament tissues involves the
 CC administration of a composition containing at least one protein
 CC selected from MP52, BMP-12 (see AAW26589) and BMP-13 (see AAW26591).
 CC The method is used for tissue (including skin) healing and repair.
 CC This is useful for treating tendonitis, carpal tunnel syndrome and
 CC other defects of traumatic or congenital origin, in cosmetic
 CC surgery and to improve fixation of tendons or ligaments to bone.
 CC The specified proteins can also be used to increase activity of other
 CC BMPs e.g. BMP-2 (see AAW26597).
 CC [Updated on 25-MAR-2003 to correct PF field.]

SQ Sequence 120 AA;

Query Match 99.4%; Score 645; DB 16; Length 120;

Query Match 99.4%; Score 645; DB 18; Length 120;
 Best Local Similarity 99.2%; Pred. No. 1.8e-59;
 Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLATROGKRPSPKLNKARCSRKALHVNFKDMGMDWMTIAPLEYAFHCEGICEFPLRSHLE 60
 DB 2 PLATROGKRPSPKLNKARCSRKALHVNFKDMGMDWMTIAPLEYAFHCEGICEFPLRSHLE 61
 QY 61 PTNHAIVQTLNNSMDPESTPPTACVPTRLSPISILFTDSANNVVKQYEDMVVESCGR 119
 DB 62 PTNHAIVQTLNNSMDPESTPPTCCVPTRLSPISILFTDSANNVVKQYEDMVVESCGR 120

RESULT 6

AAE10973
 ID AAE10973 standard; Protein; 120 AA.

XX AAE10973;

DT 18-DEC-2001 (first entry)

DE Human MP-52 protein.

KW Human; MP-52; vulnery; antiinflammatory; analgesic; ligament defect;
 KM transforming growth factor-beta; TGF-beta; tissue formation; tendonitis;
 KN wound healing; tissue repair; carpal tunnel syndrome; gene therapy.

OS Homo sapiens.

PN US6284872-B1.

PD 04-SEP-2001.

PF 28-FEB-1997; 97US-0808324.

PR 22-DEC-1994; 94US-0362670.

PR 07-DEC-1993; 93US-0164103.

PR 25-MAR-1994; 94US-0217780.

PR 02-NOV-1994; 94US-0333576.

PA (GENE) GENETICS INST INC.

PA (HARD) HARVARD COLLEGE.

PI Celeste AJ, Wozney JM, Rosen VA, Wolfman NM, Thomsen GH;

PI Melton DA;

DR WPI; 2001-588978/66.

DR N-PSDB; AAD18317.

XX New chimeric DNAs, useful for treating tendonitis, carpal tunnel

XX syndrome and other tendon and ligament defects, comprises DNA encoding

XX BMP-13 or MP52 -

XX Disclosure; Column 39-40; 42pp; English.

XX The invention relates to a chimeric DNA comprising a DNA sequence

XX encoding a propeptide of a member of the transforming growth factor

XX (TGF)-beta superfamily of proteins. This DNA is linked to a DNA sequence

XX encoding an amino acid sequence encoding a mature polypeptide consisting

XX of Bone Morphogenetic Protein (BMP)-12, BMP-13 or MP52 protein. The DNA

XX sequences are useful for producing proteins which induce tendon/ligament

XX like tissue formation, and for isolating and cloning further DNA

XX sequences encoding BMP-12 related proteins with similar activity. The

XX proteins are useful for the induction of tendon/ligament-like tissue

XX formation, wound healing, ligament and other tissue repair, augmenting

XX the activity of bone morphogenetic proteins, and for treating tendonitis,

XX carpal tunnel syndrome and other tendon and ligament defects. The

XX present sequence is human MP-52 protein.

Query Match 99.4%; Score 645; DB 22; Length 120;
 Best Local Similarity 99.2%; Pred. No. 1.8e-59;
 Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLATROGKRPSPKLNKARCSRKALHVNFKDMGMDWMTIAPLEYAFHCEGICEFPLRSHLE 60
 DB 2 PLATROGKRPSPKLNKARCSRKALHVNFKDMGMDWMTIAPLEYAFHCEGICEFPLRSHLE 61
 QY 61 PTNHAIVQTLNNSMDPESTPPTACVPTRLSPISILFTDSANNVVKQYEDMVVESCGR 119
 DB 62 PTNHAIVQTLNNSMDPESTPPTCCVPTRLSPISILFTDSANNVVKQYEDMVVESCGR 120

RESULT 7

ABG73290
 ID ABG73290 standard; Protein; 120 AA.

XX ABG73290;

DT 30-APR-2003 (first entry)

DE Amino acid sequence for human MP52.

KW Human; bone morphogenetic protein-12; BMP-12; BMP-12 related protein;
 KM BMP-13; VL-1; BMP/TGF-beta/Vg-1 family; tissue repair; tendonitis;
 KN tendon/ligament-like tissue formation; trauma induced tendon defect;
 KW tendon/ligament-like tissue healing; tendon damage; ligament damage;
 KM tendon fixation; ligament fixation; congenital; ligament defect;
 KW cosmetic plastic surgery; vulnery; MP52.

OS Homo sapiens.

PN US2002160494-A1.

PD 31-OCT-2002.

PF 31-AUG-2001; 2001US-0945182.

PR 22-DEC-1994; 94US-0362670.

PR 28-FEB-1997; 97US-0808324.

PR 07-DEC-1993; 93US-0164103.

PR 25-MAR-1994; 94US-0217780.

PR 02-NOV-1994; 94US-0333576.

XX (CELE) CELESTE A J.

XX (WOZ) WOZNEY J M.

XX (ROSE) ROSEN V A.

XX (WOLF) WOLFMAN N W.

XX (THOM) THOMSEN G H.

XX (MELT) MELTON D A.

PI Celeste AJ, Wozney JM, Rosen VA, Wolfman NM, Thomsen GH;

PI Melton DA;

DR WPI; 2003-238228/23.

DR N-PSDB; ABX11141.

XX New bone morphogenetic proteins (designated BMP-12) or related

XX proteins, useful for inducing tendon/ligament-like tissue formation in

XX a patient, or for tendon/ligament-like tissue healing or repair (e.g.

XX for treating tendonitis) -

XX Claim 26; Page 21; 46pp; English.

XX The present invention relates to the isolation of human bone

XX morphogenetic protein-12 (BMP-12) protein and a BMP-12 related protein

XX (designated BMP-13 or VL-1), and the polynucleotide sequences encoding

| | |
|---------------------------|-------------------------------------------------------------------------|
| CC | pharmaceutical composition for the treatment of various bone, cartilage |
| CC | or tooth defects and in tissue and wound repair processes. These |
| CC | proteins may also be used as immunosuppressors in organ transplants and |
| CC | in cosmetic surgery. Antibodies raised against these proteins may be |
| CC | used for diagnostic purposes. |
| CC | (updated on 25-MAR-2003 to correct PN field.) |
| CX | |
| SQ | Sequence 401 AA; |
| Query Match | 99.4%; Score 645; DB 14; Length 401; |
| Best Local Similarity | 99.2%; Pred. No. 7,8e-59; |
| Matches 118; Conservative | 0; Mismatches 1; Indels 0; Gaps |
| Dy | 1 PLATROGRPSKQLKARCCKRKALHVNFKMGWDMTIALEAFHCGLCEFPILRSHLE 60 |
| Dd | 283 PLATROGKKPPSKNLKARCCKRKALHVNFKMGMDDMTIAPLEYAFAHCGLCEFPILRSHLE 34 |
| Dy | 61 PTHNAVYIGTLNMSDESPTPACVTRTSPLSIIFISDANNVVKQYEDMVESSGCR 119 |
| Dd | 343 PTHNAVYIGTLNMSDESPTPCQVTRLSPLSIFISDANNVVKQYEDMVESSGCR 401 |
| RESULT 9 | |
| AAR69600 | |
| ID | AAR69600 standard; Protein; 501 AA. |
| XX | |
| AC | AAR69600; |
| DT | 25-MAR-2003 (updated) |
| DT | 10-OCT-1995 (first entry) |
| XX | |
| DE | New TGF-beta family member - MP-52 protein sequence. |
| KX | Transforming growth factor-beta family; mitogenic; differentiation; |
| KX | treatment; prevention; disease; bone; cartilage; connective tissue; |
| KX | skin; mucosa; epithelium; dental tissue; wound healing; osteoporosis; |
| KX | tissue regeneration; arthritis; ss. |
| OS | Homo sapiens. |
| FH | Key Location/Qualifiers |
| FT | Peptide 382 |
| FT | /label=mature protein |
| PN | M0504819-AI. |
| PD | |
| PF | 16-FEB-1995. |
| XX | |
| FF | 09-AUG-1994; 94WO-BP02630. |
| XX | |
| PR | 10-AUG-1993; 93DE-4326829. |
| PR | 25-MAY-1994; 94DE-4418222. |
| PR | 09-JUN-1994; 94DE-4420157. |
| PA | (BIOP-) BIOPHARM GBS BIOTECHNOLOGISCHEM ENTWICKL. |
| PI | Hotten G, Neithardt H, Paulista M, Hoetten G; |
| DR | WPI; 1995-090897/12. |
| DR | N-PDB; AAO83695. |
| PT | New DNA encoding a new member of the TGF beta family - and |
| PT | related vectors, host cells etc., has mitogenic and |
| PT | differentiation inducing activity, e.g. for treating or |
| PT | preventing diseases of bone and cartilage etc. |
| PS | Claim 6; Page 36; 51pp; German. |
| CC | The amino acid sequence of a novel member of the transforming growth |
| CC | factor-beta (TGF-beta) family named MP-52. The gene encodes a protein |
| CC | of 501 amino acids (AA). The protein, or at least the mature protein, |
| CC | has mitogenic and/or differentiation inducing properties useful in |
| CC | the treatment or prevention of diseases of bone, cartilage, connective |

CC tissue, skin, mucosa, epithelium or dental tissue. The protein can also
CC be used for wound healing and tissue regeneration e.g. in osteoporosis
CC and arthritis
CC (Updated on 25-MAR-2003 to correct PN field.)
CC

SQ Sequence 501 AA;

Query Match 99.4%; Score 645; DB 16; Length 501;
Best Local Similarity 99.2%; Pred. No. 1e-58;
Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLATROGKRPSSKNLAKRCSRKALHVNFKDMGMDWITAPLEVEAFHCEGLCEPPLRSHLE 60
DB 383 PLATROGKRPSSKNLAKRCSRKALHVNFKDMGMDWITAPLEVEAFHCEGLCEPPLRSHLE 442
QY 61 PTNHAIVITLNMNSMDPESTPTACVPTRLSPISILFIDSANNVYVKQYEDMVESGCR 119
DB 443 PTNHAIVITLNMNSMDPESTPTACVPTRLSPISILFIDSANNVYVKQYEDMVESGCR 501

RESULT 10

AAW36100
ID AAW36100 standard; Protein; 501 AA.

AC AAW36100;
DT 08-MAY-1998 (first entry)
DE Human MP52.

KW Bone morphogenetic protein; BMP; processing enzyme; MP52;
KW BMP-2; BMP-4; BMP-6; BMP-7; bone formation; bone regeneration.
OS Homo sapiens.

EN M09741250-A1.

PD 06-NOV-1997.

PF 28-APR-1997; 97WO-JP01474.

PR 30-APR-1996; 96JP-0130618.

PA (FARH) HOECHST YAKUHIN KOGYO KK.
PA (FARH) HOECHST PHARM & CHEM KK.

PI Kimura M, Makishima F, Takahashi M,

WPI; 1997-549748/50.

DR N-PSDB; AAT98191.

PT Production of mature bone morphogenetic protein - by treatment of
PT precursor protein with a processing enzyme such as furin either
PT directly or by expressing them both in the same host

PS Example 1; Pages 21-25; 34pp; Japanese.

CC The present sequence is MP52, which is a bone morphogenetic
CC protein (BMP).

CC Mature BMP can be produced by directly adding a BMP processing
CC enzyme to a solution containing BMP precursor protein, or by
CC transforming an animal cell with expression vectors containing DNA
CC encoding the enzyme and precursor protein, culturing the
CC transformant and isolating the mature BMP from the culture. The
CC method can be used to produce MP52, BMP-2, BMP-4, BMP-6 and BMP-7,
CC which can be used to treat bone formation or regeneration
CC abnormalities.

SQ Sequence 501 AA;

Query Match 99.4%; Score 645; DB 18; Length 501;
Best Local Similarity 99.2%; Pred. No. 1e-58;
Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLATROGKRPSSKNLAKRCSRKALHVNFKDMGMDWITAPLEVEAFHCEGLCEPPLRSHLE 60
DB 383 PLATROGKRPSSKNLAKRCSRKALHVNFKDMGMDWITAPLEVEAFHCEGLCEPPLRSHLE 442
QY 61 PTNHAIVITLNMNSMDPESTPTACVPTRLSPISILFIDSANNVYVKQYEDMVESGCR 119
DB 443 PTNHAIVITLNMNSMDPESTPTACVPTRLSPISILFIDSANNVYVKQYEDMVESGCR 501

RESULT 11

AAW19210
ID AAW19210 standard; Protein; 501 AA.

AC AAW19210;

DT 04-MAR-1998 (first entry)

DE Human TGF-beta protein MP52.

KW Human transforming growth factor-beta; TGF-beta; MP52; superfamily;
KW cartilage; bone inducing activity; inhibic; bone resorption.

OS Homo sapiens.

EN DE19548476-A1.

PD 26-JUN-1997.

PF 22-DEC-1995; 95DE-1048476.

PR 22-DEC-1995; 95DE-1048476.

PA (RIOP-) BIOPHARM GBS BIOTECHNOLOGISCHE ENTWICKL.

PI Bechtold R, Hotten G, Paulista M, Fohl J, Heerten G,

WPI; 1997-333931/31.

DR N-PSDB; AAT69695.

PT Compound containing protein from TGF-beta superfamily - has bone
PT and/or cartilage inducing activity, useful in treatment of, e.g.
PT osteoporosis, bone damage, Paget's disease and osteoarthritis
PS Claim 3; Page 9; 10pp; German.

CC This sequence is the human transforming growth factor (TGF)-beta protein
CC designated MP52. MP52 can be used in a compound of formula (I):
CC A-X(1-20)-B(1-20) (I; A = protein, or fragment, of the TGF-beta
CC superfamily with cartilage and/or bone inducing activity (e.g. MP52);
CC B = 1 or more substituent groups with an affinity to the extracellular
CC matrix, cellular components of bone and/or cartilage and/or to a
CC biocompatible carrier matrix; X = 1 or more covalent bonds and/or spacer
CC groups. The compound may be used to inhibit bone resorption, prevent or
CC treat bone or cartilage related disorders, including osteoporosis,
CC Paget's disease, osteodystrophy, osteoarthritis or osteoarthropathy and
CC to treat bone or cartilage damage caused by wounding or overloading.

SQ Sequence 501 AA;

Query Match 99.4%; Score 645; DB 18; Length 501;
Best Local Similarity 99.2%; Pred. No. 1e-58;
Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLATROGKRPSSKNLAKRCSRKALHVNFKDMGMDWITAPLEVEAFHCEGLCEPPLRSHLE 60
DB 383 PLATROGKRPSSKNLAKRCSRKALHVNFKDMGMDWITAPLEVEAFHCEGLCEPPLRSHLE 442
QY 61 PTNHAIVITLNMNSMDPESTPTACVPTRLSPISILFIDSANNVYVKQYEDMVESGCR 119
DB 443 PTNHAIVITLNMNSMDPESTPTACVPTRLSPISILFIDSANNVYVKQYEDMVESGCR 501

```

RESULT 12
AAW11900
ID AAW11900 standard; Protein; 501 AA.
XX
AC AAW11900;
XX
DT 28-OCT-1997 (first entry)
XX
DE Human high mol. wt. protein MP52, a growth/differentiation factor.
XX
KW Growth factor; differentiation; bone induction; osteoporosis; teeth;
KW tooth; dental; joint tissue; cartilage; mucous membrane; skin; nails;
KW wound healing; regeneration; skeletal disorder; fracture; dimer.
XX
OS Homo sapiens.
XX
PN WO9704095-A1.
XX
PD 06-FEB-1997.
XX
PF 24-JUL-1996; 96WO-UP02065.
XX
PR 24-JUL-1995; 95JP-0218022.
XX
PA (FAH) HOECHST JAPAN LTD.
XX
PA (FAH) HOECHST PHARM & CHEM KK.
XX
PI Fujino Y, Kawai S, Kimura M, Matsumoto T, Takahashi M;
XX
DR WPI; 1997-132636/12.
XX
DR N-PSDB; AAT61412.
XX
PT High molecular weight human MP52 growth or differentiation factor -
PT promotes bone induction, is useful for treatment and prevention of
PT bone disease
XX
PS Claim 1; Page 12-16; 25pp; Japanese.
XX
CC AAW11900 is a high mol. wt. form of a human growth/differentiation
CC factor MP52. MP52 promotes bone induction and is useful for plastic
CC reconstructive surgery, cosmetic facial treatment, bone transplantation
CC and tooth implantation. It is also useful for the treatment and
CC prevention of disorders of bone formation, bone, cartilage, joint
CC tissue, skin, mucous membranes, nails or teeth for wound treatment and
CC tissue regeneration; and for the treatment of skeletal disorders and
CC fractures.
XX
SQ Sequence 501 AA;
XX
Query Match 99.4%; Score 645; DB 18; Length 501;
Best Local Similarity 99.2%; Pred. No. 1e-58;
Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 PLATROGKRPSKNIKARCSRKALHVNFKDMGMDWIIAPLEYEAFHCGCEPFLRSHTL 60
DB 383 PLATROGKRPSKNIKARCSRKALHVNFKDMGMDWIIAPLEYEAFHCGCEPFLRSHTL 442
OY 61 PTNHAVIQTLNMSMDPESTPTACVPTRLSPISILFTDSANNVYKQYEDVWVSCGCR 119
DB 443 PTNHAVIQTLNMSMDPESTPTACVPTRLSPISILFTDSANNVYKQYEDVWVSCGCR 501
RESULT 13
AAW01799
ID AAW01799 standard; Protein; 501 AA.
XX
AC AAW01799;
XX
DT 15-OCT-1997 (first entry)
XX
DE Human MP52 protein.
XX
KW Human; MP52; transforming growth factor; TGF; beta; medicament;

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KW treatment; prevention; nervous system; disease; neuropathology;
KW ageing.
XX
OS Homo sapiens.
XX
PN DE19525416-A1.
XX
PD 16-JAN-1997.
XX
PF 12-JUL-1995; 95DE-1025416.
XX
PR 12-JUL-1995; 95DE-1025416.
XX
PA (BIOP-) BIOPHARM GES BIOTECHNOLOGISCHEN ENTWICKL.
XX
PI Bechtold R, Hoetten G, Paulista M, Pohl J, Unsicker K;
XX
DR WPI; 1997-078343/08.
XX
DR N-PSDB; AAT59405.
XX
PT Medicaments contg. protein MP52 - useful for treating neurological
PT disorders
XX
PS Claim 2; Pages 12-14; 21pp; German.
XX
CC The present sequence is the human MP52 protein, which is
CC described in WO 9316099 and 9504819 as a member of the human
CC transforming growth factor beta superfamily. Active MP52 can be
CC used in a medicament to treat and prevent nervous system diseases,
CC and/or to treat neuropathological conditions caused by nervous
CC system ageing.
XX
SQ Sequence 501 AA;
XX
Query Match 99.4%; Score 645; DB 18; Length 501;
Best Local Similarity 99.2%; Pred. No. 1e-58;
Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 PLATROGKRPSKNIKARCSRKALHVNFKDMGMDWIIAPLEYEAFHCGCEPFLRSHTL 60
DB 383 PLATROGKRPSKNIKARCSRKALHVNFKDMGMDWIIAPLEYEAFHCGCEPFLRSHTL 442
OY 61 PTNHAVIQTLNMSMDPESTPTACVPTRLSPISILFTDSANNVYKQYEDVWVSCGCR 119
DB 443 PTNHAVIQTLNMSMDPESTPTACVPTRLSPISILFTDSANNVYKQYEDVWVSCGCR 501
RESULT 14
AAW12770
ID AAW12770 standard; Protein; 501 AA.
XX
AC AAW12770;
XX
DT 11-MAY-1997 (first entry)
XX
DE Human bone morphogenic factor MP52 Arg.
XX
KW Bone morphogenic factor; MP52 Arg; bone; cartilage; skin;
KW connective tissue; mucous membrane; epithelium; teeth;
KW wound healing; vulnery; tissue regeneration; osteoporosis;
KW bone fracture; dental implant; osteoblast.
XX
OS Homo sapiens.
XX
PN Key Location/Qualifiers
XX
FT Peptide 1..27
FT /label= Sig_peptide
FT Cleavage-site 380..381
FT /note= "sequencing suggests MP52 Arg is processed
FT /note= proteolytically at Arg380-Arg381"
FT Cleavage-site 381..382
FT /note= "alternative cleavage site at Arg381-Ala382"
FT Mat_protein 381..501

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FT FT /label= Mat_protein
FT FT /note= "mature MP52 Arg preferred for use in
XX XX compns. of the invention"
XX XX
XX WO9706254-A1.
XX
XX 20-FEB-1997.
XX
XX 02-AUG-1996; 96WO-EP03427.
XX
XX 03-AUG-1995; 95EP-0112241.
XX
XX (BIOP-) BIOPHARM GES BIOTECHNOLOGISCHEN ENTWICKLUNG.
XX
XX Fujino Y, Kawai S, Kimura M, Matsumoto T, Takahashi M;
XX
XX WPI; 1997-154261/14.
XX
XX N-PSDB; AAT59729.
XX
XX New human bone morphogenic factor, MP52 Arg - used in the treatment
XX of osteoporosis and bone fracture, and for promoting bone regrowth
XX
XX Claim 1; Page 12-15; 26pp; English.
XX
XX Novel human bone morphogenic factor MP52 Arg (AAW12770) is a growth
XX factor that induces formation of cartilage from undifferentiated
XX mesenchymal cells and which stimulates the differentiation and
XX maturation of osteoblasts. It is effective for treating/preventing
XX bone diseases caused by abnormal bone metabolism such as
XX osteoporosis. It also accelerates the healing of bone fractures,
XX and is useful for orthopaedic reconstruction, bone transplantation,
XX CC and dental therapeutics because of its bone morphogenetic activity.
XX CC It is also effective for preventing/treating cartilage, skin,
XX CC connective tissue, mucous membrane, teeth and epithelial disorders.
XX CC Recombinant MP52 Arg can be produced in host (e.g. CHO) cells
XX CC utilizing an isolated DNA sequence (AAT59729) in plasmid pMS59.
XX
XX Sequence 501 AA:
SQ
XX
XX Query Match 99.4%; Score 645; DB 18; Length 501;
XX Best Local Similarity 99.2%; Pred. No. 1e-58;
XX Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1 PLATROGKRSPSKNLKARCSRKALHVNFKDMGMDMIAPLEYEAFHCEGLCEPPLRSHLT 60
XX DB 383 PLATROGKRSPSKNLKARCSRKALHVNFKDMGMDMIAPLEYEAFHCEGLCEPPLRSHLT 442
XX
XX QY 61 PTNHAVIQTLMNSMDPESTPTACVPTRLSPISILFTDSANNVYKQYEDMVVESCGR 119
XX DB 443 PTNHAVIQTLMNSMDPESTPTCCVPTRLSPISILFTDSANNVYKQYEDMVVESCGR 501
XX
XX RESULT 15
XX AAW44868
XX ID AAW44868 standard; protein; 501 AA.
XX
XX AC AAW44868;
XX
XX 24-SEP-1998 (first entry)
XX
XX TGF-beta superfamily subunit.
XX
XX TGF-beta; calcium phosphate matrix; bioactive implant; parodontosis;
XX KW bone replacement; cartilage; bone; fracture.
XX
XX Synthetic.
XX
XX DE19647853-A1.
XX
XX 20-MAY-1998.
XX
XX 19-NOV-1996; 96DE-1047853.
XX

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```

PR 19-NOV-1996; 96DE-1047853.
XX
XX (BIOP-) BIOPHARM GES BIOTECHNOLOGISCHEN ENTWICKL.
XX
XX (GERO-) GERONTOCARE GMBH BIOMATERIALS & MEDICAL.
XX
XX Heide H, Pabst J, Paulista M, Pohl J;
XX
XX WPI; 1998-287890/26.
XX
XX Bioactive implant material for bone replacement - comprising
XX PT osteogenic calcium phosphate matrix coated with protein
XX
XX Claim 3; Page 8-10; 12pp; German.
XX
XX The TGF-beta superfamily subunit can be used together with a calcium
XX CC phosphate matrix to produce a bioactive implant material for bone
XX CC replacement. The implant has cartilage and/or bone-forming activity and
XX CC can be used for local treatment of cartilage and/or bone diseases or
XX CC damage caused by trauma, surgery, degeneration or overloading. The
XX CC implant can also be used for the treatment of bone defects, e.g.
XX CC parodontosis or fractures and in cosmetic and plastic surgery for fixing
XX CC mobile bones.
XX
XX Sequence 501 AA:
SQ
XX
XX Query Match 99.4%; Score 645; DB 19; Length 501;
XX Best Local Similarity 99.2%; Pred. No. 1e-58;
XX Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1 PLATROGKRSPSKNLKARCSRKALHVNFKDMGMDMIAPLEYEAFHCEGLCEPPLRSHLT 60
XX DB 383 PLATROGKRSPSKNLKARCSRKALHVNFKDMGMDMIAPLEYEAFHCEGLCEPPLRSHLT 442
XX
XX QY 61 PTNHAVIQTLMNSMDPESTPTACVPTRLSPISILFTDSANNVYKQYEDMVVESCGR 119
XX DB 443 PTNHAVIQTLMNSMDPESTPTCCVPTRLSPISILFTDSANNVYKQYEDMVVESCGR 501
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Search completed: February 18, 2004, 17:42:06
Job time : 41 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 18, 2004, 17:43:25 ; Search time 34 Seconds

(without alignments)
732.838 Million cell updates/sec

Title: US-09-701-121-2

Perfect score: 649
Sequence: 1 FIAPRQGRPSKMLKARCSR.....ANNVYKQEDMVYESGCR 119

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 801455 seqs, 209382283 residues

Total number of hits satisfying chosen parameters: 801455

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

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18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|------------------|
| 1 | 645 | 99.4 | 119 | 8 | US-08-945-459A-1 |
| 2 | 645 | 99.4 | 119 | 8 | US-09-068-253-2 |
| 3 | 645 | 99.4 | 119 | 12 | US-10-365-231-1 |
| 4 | 645 | 99.4 | 119 | 12 | US-10-414-954-1 |
| 5 | 645 | 99.4 | 120 | 10 | US-09-945-182-4 |
| 6 | 645 | 99.4 | 501 | 8 | US-08-981-490B-1 |
| 7 | 645 | 99.4 | 501 | 12 | US-10-164-279-53 |
| 8 | 645 | 99.4 | 501 | 12 | US-10-356-513-1 |
| 9 | 645 | 99.4 | 501 | 12 | US-10-356-513-5 |
| 10 | 640 | 98.6 | 119 | 10 | US-09-880-708-13 |
| 11 | 640 | 98.6 | 495 | 10 | US-09-880-708-10 |
| 12 | 639 | 98.5 | 502 | 10 | US-09-813-398-37 |
| 13 | 629 | 96.9 | 501 | 9 | US-09-730-772-13 |
| 14 | 629 | 96.9 | 501 | 9 | US-09-735-849-13 |
| 15 | 629 | 96.9 | 501 | 12 | US-10-379-830-13 |

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| 16 | 629 | 96.9 | 501 | 12 | US-09-574-819-13 | Sequence 13, Appl |
| 17 | 548 | 84.4 | 354 | 12 | US-09-930-512-74 | Sequence 76, Appl |
| 18 | 540 | 83.2 | 321 | 10 | US-09-945-182-26 | Sequence 26, Appl |
| 19 | 540 | 83.2 | 455 | 12 | US-09-930-512-20 | Sequence 20, Appl |
| 20 | 540 | 83.2 | 455 | 12 | US-10-297-639-6 | Sequence 6, Appl |
| 21 | 538 | 82.9 | 263 | 10 | US-09-945-182-32 | Sequence 32, Appl |
| 22 | 528 | 81.4 | 436 | 9 | US-09-730-772-14 | Sequence 14, Appl |
| 23 | 528 | 81.4 | 436 | 12 | US-09-735-849-14 | Sequence 14, Appl |
| 24 | 528 | 81.4 | 436 | 12 | US-10-379-830-14 | Sequence 14, Appl |
| 25 | 528 | 81.4 | 436 | 12 | US-09-574-819-14 | Sequence 14, Appl |
| 26 | 528 | 81.4 | 436 | 12 | US-10-164-279-57 | Sequence 57, Appl |
| 27 | 528 | 81.4 | 436 | 12 | US-09-930-512-72 | Sequence 72, Appl |
| 28 | 527 | 81.2 | 413 | 12 | US-09-930-512-76 | Sequence 76, Appl |
| 29 | 524 | 80.7 | 399 | 12 | US-09-930-512-73 | Sequence 73, Appl |
| 30 | 524 | 80.7 | 412 | 12 | US-09-930-512-75 | Sequence 75, Appl |
| 31 | 494 | 76.1 | 294 | 10 | US-09-945-182-2 | Sequence 2, Appl |
| 32 | 494 | 76.1 | 388 | 10 | US-09-945-182-34 | Sequence 34, Appl |
| 33 | 494 | 76.1 | 411 | 10 | US-09-945-182-28 | Sequence 28, Appl |
| 34 | 494 | 76.1 | 450 | 15 | US-10-188-246-12 | Sequence 12, Appl |
| 35 | 493 | 76.0 | 151 | 12 | US-10-164-279-61 | Sequence 61, Appl |
| 36 | 489 | 75.3 | 240 | 10 | US-09-945-182-30 | Sequence 30, Appl |
| 37 | 385 | 59.3 | 72 | 10 | US-09-945-182-15 | Sequence 15, Appl |
| 38 | 348 | 53.6 | 72 | 10 | US-09-945-182-13 | Sequence 13, Appl |
| 39 | 347 | 53.5 | 117 | 14 | US-10-115-406-13 | Sequence 13, Appl |
| 40 | 347 | 53.5 | 117 | 15 | US-10-154-333-15 | Sequence 15, Appl |
| 41 | 347 | 53.5 | 118 | 10 | US-09-813-459-10 | Sequence 10, Appl |
| 42 | 347 | 53.5 | 118 | 10 | US-09-859-211-37 | Sequence 37, Appl |
| 43 | 347 | 53.5 | 118 | 10 | US-09-880-708-15 | Sequence 15, Appl |
| 44 | 347 | 53.5 | 118 | 11 | US-09-872-856-37 | Sequence 37, Appl |
| 45 | 347 | 53.5 | 118 | 15 | US-10-335-483-19 | Sequence 19, Appl |

ALIGNMENTS

RESULT 1
US-08-945-459A-1
; Sequence 1, Application US/08945459A
; Publication No. US20020102633A1
GENERAL INFORMATION:
APPLICANT: MAKISHIMA, FUSAO; TAKAMATSU,
APPLICANT: HIROTSUKI, MIKI; HIDEO, KAWAI,
APPLICANT: SHIMIZU, KIMURA, MICHIO; MATSUMOTO,
APPLICANT: TOMOKI, KATSURA, MIEKO; ENOMOTO,
APPLICANT: KOICHI; SATOH, YUSUKE
TITLE OF INVENTION: A NOVEL PROTEIN AND
TITLE OF INVENTION: PROCESS FOR PREPARING THE SAME
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESS: BIERMAN, MUSERLIAN AND LUCAS
ADDRESS: LLP
STREET: 600 THIRD AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MICROSOFT WORD 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/945, 459A
FILING DATE: 09-DEC-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP96/01062
FILING DATE: 19-APR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP7/322403
FILING DATE: 17-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP7/93664
FILING DATE: 19-APR-1995

ATTORNEY/AGENT INFORMATION:
NAME: CHARLES A. MUSERLIAN
REGISTRATION NUMBER: 19,683
REFERENCE/DOCKET NUMBER: 146.1275
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 661-8000
TELEFAX: (212) 661-8002
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 AMINO ACIDS
TYPE: AMINO ACID
STRANDEDNESS:
TOPOLOGY: LINEAR
MOLECULE TYPE: PEPTIDE
ORIGINAL SOURCE:
ORGANISM: HOMOSAPIENS
TISSUE TYPE: FETUS
FEATURE:
NAME/KEY: MP52
LOCATION: 383 TO 501
US-08-945-459A-1

Query Match 99.4%; Score 645; DB 8; Length 119;
Best Local Similarity 99.2%; Pred. No. 1.8e-62;
Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLATGGRPSKNTLKARCSRKALHVNFKDMGMDMIAPLEYAFHCGGLCEFPILRSILE 60
DB 1 PLATGGRPSKNTLKARCSRKALHVNFKDMGMDMIAPLEYAFHCGGLCEFPILRSILE 60
QY 61 PTNHAVIQTLNMSMDPESTPTPCVPTLSPISILFIDSANVVKQYEDMVVESCGR 119
DB 61 PTNHAVIQTLNMSMDPESTPTPCVPTLSPISILFIDSANVVKQYEDMVVESCGR 119

RESULT 2

US-09-068-253-2
Sequence 2, Application US/09068253
Patent No. US2002016831A1
GENERAL INFORMATION:
APPLICANT: SHIMURA, Takesada
TITLE OF INVENTION: CARTILAGE/ BONE INDUCING MATERIALS FOR REPARATION
FILE REFERENCE: 146.1286
CURRENT APPLICATION NUMBER: US/09/068,253
CURRENT FILING DATE: 1998-06-09
PRIOR APPLICATION NUMBER: PCT/JP96/03333
PRIOR FILING DATE: 1996-11-14
PRIOR APPLICATION NUMBER: JP 7/322402
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 119
TYPE: PRT
ORGANISM: Homo sapiens
US-09-068-253-2

Query Match 99.4%; Score 645; DB 10; Length 119;
Best Local Similarity 99.2%; Pred. No. 1.8e-62;
Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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RESULT 3

US-10-365-231-1
Sequence 1, Application US/10365231
Publication No. US20030181378A1
GENERAL INFORMATION:
APPLICANT: MAKISHIMA, FUSAO; TAKAMATSU,
HIROYUKI; MIKI, HIDEO; KAWAI,
SHINGJI; KIMURA, MICHIO; MATSUMOTO,
TOMOKI; KATSURA, MIEKO; ENOMOTO,
KOICHI; SATOH, YUSUKE
TITLE OF INVENTION: A NOVEL PROTEIN AND
PROCESS FOR PREPARING THE SAME
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIERMAN, MUSERLIAN AND LUCAS
LLP
STREET: 600 THIRD AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MICROSOFT WORD 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/365,231
FILING DATE: 12-Feb-2003
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP96/01062
FILING DATE: 19-APR-1996
APPLICATION NUMBER: JP7/322403
FILING DATE: 17-NOV-1995
APPLICATION NUMBER: JP7/93664
FILING DATE: 19-APR-1995

ATTORNEY/AGENT INFORMATION:
NAME: CHARLES A. MUSERLIAN
REGISTRATION NUMBER: 19,683
REFERENCE/DOCKET NUMBER: 146.1275
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 661-8000
TELEFAX: (212) 661-8002
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 AMINO ACIDS
TYPE: AMINO ACID
STRANDEDNESS: <Unknown>
TOPOLOGY: LINEAR
MOLECULE TYPE: PEPTIDE
ORIGINAL SOURCE:
ORGANISM: HOMOSAPIENS
TISSUE TYPE: FETUS
FEATURE:
NAME/KEY: MP52
LOCATION: 383 TO 501
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-365-231-1

Query Match 99.4%; Score 645; DB 12; Length 119;
Best Local Similarity 99.2%; Pred. No. 1.8e-62;
Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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RESULT 4

US-10-414-954-1
; Sequence 1, Application US/10414954
; Publication No. US2004019185A1
; GENERAL INFORMATION:
; APPLICANT: ANDOU, HIDEOSHI
; APPLICANT: HONDA, JUN
; APPLICANT: SUGIMOTO, SUTUNIRO
; APPLICANT: HOTTEN, GETRUD
; APPLICANT: BECHTOLD, ROLF
; APPLICANT: POHL, JENS
; TITLE OF INVENTION: PROCESS FOR PREPARING PURIFIED ACTIVE MONOMER OF
; FILE REFERENCE: 146:1320-1
; CURRENT APPLICATION NUMBER: US/10/414,954
; PRIOR FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: 10/048,458
; PRIOR FILING DATE: 2002-02-26
; PRIOR APPLICATION NUMBER: 09/701,121
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: PCT/EP00/07600
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: 09/331,948
; PRIOR FILING DATE: 1999-06-24
; PRIOR APPLICATION NUMBER: JP 10 141379
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: PCT/JP97/04784
; PRIOR FILING DATE: 1997-12-24
; PRIOR APPLICATION NUMBER: JP 8 355812
; PRIOR FILING DATE: 1996-12-25
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: human MP52
; OTHER INFORMATION: variant
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (83)
; OTHER INFORMATION: if dimeric human MP52 variant, Xaa is cysteine; if
; OTHER INFORMATION: monomeric human MP52 variant, Xaa is any amino acid
; OTHER INFORMATION: except cysteine and preferably alanine, serine,
; OTHER INFORMATION: threonine, leucine, isoleucine, glycine or valine
US-10-414-954-1
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Best Local Similarity 99.2%; Pred. No. 1.8e-62;
Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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DB 61 PTNNAVIQTLNMSMDPESTPTPTACVPTRLSPISIIIFIDSANNVYKQYEDMVVESCGR 119
RESULT 5
US-09-945-182-4
; Sequence 4, Application US/09945182
; Patent No. US20020160494A1
; GENERAL INFORMATION:
; APPLICANT: Celestre, Anthony J.
; APPLICANT: Mooney, John
; APPLICANT: Rosen, Vicki A.
; APPLICANT: Koltman, Neil
; APPLICANT: Thomsen, Gerald H.
; APPLICANT: Melton, Douglas A.
; TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS
; NUMBER OF SEQUENCES: 35

CORRESPONDENCE ADDRESS:
ADDRESSEE: GENETICS INSTITUTE, INC.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: USA
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/945,182
FILING DATE: 31-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/808,324
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Lazar, Steven R.
REGISTRATION NUMBER: 32,618
REFERENCE/DOCKET NUMBER: 5202-D
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617 498-8260
TELEFAX: 617 876-5851
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-945-182-4
Query Match 99.4%; Score 645; DB 10; Length 120;
Best Local Similarity 99.2%; Pred. No. 1.8e-62;
Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 PLATGGRPSKNTLKARCSRKALHNFKDGMWDWIIAPLEYEAFHCGLCPEPLRSILE 60
DB 2 PLATGGRPSKNTLKARCSRKALHNFKDGMWDWIIAPLEYEAFHCGLCPEPLRSILE 61
QY 61 PTNNAVIQTLNMSMDPESTPTPTACVPTRLSPISIIIFIDSANNVYKQYEDMVVESCGR 119
DB 62 PTNNAVIQTLNMSMDPESTPTPTACVPTRLSPISIIIFIDSANNVYKQYEDMVVESCGR 120
RESULT 6
US-08-961-490B-1
; Sequence 1, Application US/08981490B
; Publication No. US20020045568A1
; GENERAL INFORMATION:
; APPLICANT: Hotten, Gertrud
; APPLICANT: Pohl, Jens
; APPLICANT: Bechtold, Rolf
; APPLICANT: Paulister, Michael
; APPLICANT: Unsicker, Klaus
; TITLE OF INVENTION: USE OF MP52 OR MP121 FOR TREATING AND PREVENTING DISEASES OF THE
; FILE REFERENCE: 100564-07032
; CURRENT APPLICATION NUMBER: US/08/981,490B
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: PCT/EP96/03065
; PRIOR FILING DATE: 1996-07-12
; PRIOR APPLICATION NUMBER: DE/195 25 416.3
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 501
; TYPE: PRT
; ORGANISM: Homo sapiens

US-08-981-490B-1

Query Match 99.4%; Score 645; DB 8; Length 501;
Best Local Similarity 99.2%; Pred. No. 9.2e-62;
Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLATROGKRPSSKNLAKCRSKALHVNFKDGMWDMIIAPLEYAFHCEGLCEPPLRSHLE 60
DB 383 PLATROGKRPSSKNLAKCRSKALHVNFKDGMWDMIIAPLEYAFHCEGLCEPPLRSHLE 442
QY 61 PTNHAVIQTLMNSMDPESTPTCCVPTRLSPISILFIDSANNVYKQYEDMVVSCGCR 119
DB 443 PTNHAVIQTLMNSMDPESTPTCCVPTRLSPISILFIDSANNVYKQYEDMVVSCGCR 501

RESULT 7

US-10-164-279-53
Sequence 53, Application US/10164279
Publication No. US20030185792A1
GENERAL INFORMATION:
APPLICANT: Keck, P.
TITLE OF INVENTION: MORPHOGEN ANALOGS OF BOND MORPHOGENIC PROTEINS
FILE REFERENCE: CIBT-P04-566
CURRENT APPLICATION NUMBER: US/10/164,279
CURRENT FILING DATE: 2002-06-06
PRIOR APPLICATION NUMBER: 09/791946
PRIOR FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 64
SOFTWARE: PatentIn version 3.1
SEQ ID NO 53
LENGTH: 501
TYPE: PRT
ORGANISM: Homo sapiens
US-10-164-279-53

Query Match 99.4%; Score 645; DB 12; Length 501;
Best Local Similarity 99.2%; Pred. No. 9.2e-62;
Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLATROGKRPSSKNLAKCRSKALHVNFKDGMWDMIIAPLEYAFHCEGLCEPPLRSHLE 60
DB 383 PLATROGKRPSSKNLAKCRSKALHVNFKDGMWDMIIAPLEYAFHCEGLCEPPLRSHLE 442
QY 61 PTNHAVIQTLMNSMDPESTPTCCVPTRLSPISILFIDSANNVYKQYEDMVVSCGCR 119
DB 443 PTNHAVIQTLMNSMDPESTPTCCVPTRLSPISILFIDSANNVYKQYEDMVVSCGCR 501

RESULT 8

US-10-356-513-1
Sequence 1, Application US/10356513
Publication No. US20030220248A1
GENERAL INFORMATION:
APPLICANT: Hotten, Gertrud
APPLICANT: Pohl, Jens
APPLICANT: Bechtold, Rolf
APPLICANT: Paulista, Michael
APPLICANT: Unsicker, Klaus
TITLE OF INVENTION: The Use Of MP52 Or MP121 For Treating And Preventing Diseases Of
TITLE OF INVENTION: The Nervous System
FILE REFERENCE: 2923-0127
CURRENT APPLICATION NUMBER: US/10/356,513
CURRENT FILING DATE: 2003-02-03
PRIOR APPLICATION NUMBER: US 08/981490
PRIOR FILING DATE: 1998-05-18
PRIOR APPLICATION NUMBER: PCT/EP96/03065
PRIOR FILING DATE: 1996-07-12
PRIOR APPLICATION NUMBER: DE 195 25 416 .3
PRIOR FILING DATE: 1995-07-12
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn version 3.2
SEQ ID NO 1
LENGTH: 501

TYPE: PRT
ORGANISM: Human
US-10-356-513-1

Query Match 99.4%; Score 645; DB 12; Length 501;
Best Local Similarity 99.2%; Pred. No. 9.2e-62;
Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLATROGKRPSSKNLAKCRSKALHVNFKDGMWDMIIAPLEYAFHCEGLCEPPLRSHLE 60
DB 383 PLATROGKRPSSKNLAKCRSKALHVNFKDGMWDMIIAPLEYAFHCEGLCEPPLRSHLE 442
QY 61 PTNHAVIQTLMNSMDPESTPTCCVPTRLSPISILFIDSANNVYKQYEDMVVSCGCR 119
DB 443 PTNHAVIQTLMNSMDPESTPTCCVPTRLSPISILFIDSANNVYKQYEDMVVSCGCR 501

RESULT 9

US-10-356-513-5
Sequence 5, Application US/10356513
Publication No. US20030220248A1
GENERAL INFORMATION:
APPLICANT: Hotten, Gertrud
APPLICANT: Pohl, Jens
APPLICANT: Bechtold, Rolf
APPLICANT: Paulista, Michael
APPLICANT: Unsicker, Klaus
TITLE OF INVENTION: The Use Of MP52 Or MP121 For Treating And Preventing Diseases Of
TITLE OF INVENTION: The Nervous System
FILE REFERENCE: 2923-0127
CURRENT APPLICATION NUMBER: US/10/356,513
CURRENT FILING DATE: 2003-02-03
PRIOR APPLICATION NUMBER: US 08/981490
PRIOR FILING DATE: 1998-05-18
PRIOR APPLICATION NUMBER: PCT/EP96/03065
PRIOR FILING DATE: 1996-07-12
PRIOR APPLICATION NUMBER: DE 195 25 416 .3
PRIOR FILING DATE: 1995-07-12
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn version 3.2
SEQ ID NO 5
LENGTH: 501
TYPE: PRT
ORGANISM: Human
US-10-356-513-5

Query Match 99.4%; Score 645; DB 12; Length 501;
Best Local Similarity 99.2%; Pred. No. 9.2e-62;
Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLATROGKRPSSKNLAKCRSKALHVNFKDGMWDMIIAPLEYAFHCEGLCEPPLRSHLE 60
DB 383 PLATROGKRPSSKNLAKCRSKALHVNFKDGMWDMIIAPLEYAFHCEGLCEPPLRSHLE 442
QY 61 PTNHAVIQTLMNSMDPESTPTCCVPTRLSPISILFIDSANNVYKQYEDMVVSCGCR 119
DB 443 PTNHAVIQTLMNSMDPESTPTCCVPTRLSPISILFIDSANNVYKQYEDMVVSCGCR 501

RESULT 10

US-09-880-708-13
Sequence 13, Application US/09880708
Patent No. US20020165361A1
GENERAL INFORMATION:
APPLICANT: Lee, Se-Jin
APPLICANT: Huynh, Thanh
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-5
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Gray Cary Ware & Freidenrich LLP
STREET: 4365 Executive Drive, Suite 1600
CITY: San Diego
STATE: CA

```

; COUNTRY: USA
; ZIP: 92121-2189
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/880,708
; FILING DATE: 12-Jun-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/145,060
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/003,144
; FILING DATE: 12-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Lisa A. Halle, Ph.D.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07265/057002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 858/677-1456
; TELEFAX: 619/677-1465
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; IMMEDIATE SOURCE:
; CLONE: GDF-5
; SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-880-708-13

Query Match      98.6%; Score 640; DB 10; Length 119;
Best Local Similarity 98.3%; Pred. No. 6,3e-62;
Matches 117; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Cy 1 PLATROGKRPSSKLNKARCSRKALHVNFKDMGMDMTIAPLEYAFHCGGLCEPPLRSHTL 60
Db 1 PLNRQGRPSKLNKARCSRKALHVNFKDMGMDMTIAPLEYAFHCGGLCEPPLRSHTL 60
Cy 61 PTNNAVIGTLMNSMDPESTPTACVPTRLSPISILFTDSANNVYKQYEDMVVSCGCR 119
Db 61 PTNNAVIGTLMNSMDPESTPTCCVPTRLSPISILFTDSANNVYKQYEDMVVSCGCR 119

RESULT 11
US-09-880-708-10
; Sequence 10, Application US/09880708
; Patent No. US20020165361A1
; GENERAL INFORMATION:
; APPLICANT: Lee, Se-jin
; Huynh, Thanh
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-5
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Gray Cary Ware & Freidenrich LLP
; STREET: 4365 Executive Drive, Suite 1600
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92121-2189
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/880,708
; FILING DATE: 12-Jun-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/145,060
; FILING DATE: <Unknown>
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; APPLICATION NUMBER: 08/003,144
; FILING DATE: 12-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Lisa A. Halle, Ph.D.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07265/057002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 858/677-1456
; TELEFAX: 619/677-1465
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 495 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-880-708-10

Query Match      98.6%; Score 640; DB 10; Length 495;
Best Local Similarity 98.3%; Pred. No. 3,2e-61;
Matches 117; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Cy 1 PLATROGKRPSSKLNKARCSRKALHVNFKDMGMDMTIAPLEYAFHCGGLCEPPLRSHTL 60
Db 377 PLNRQGRPSKLNKARCSRKALHVNFKDMGMDMTIAPLEYAFHCGGLCEPPLRSHTL 436
Cy 61 PTNNAVIGTLMNSMDPESTPTACVPTRLSPISILFTDSANNVYKQYEDMVVSCGCR 119
Db 437 PTNNAVIGTLMNSMDPESTPTCCVPTRLSPISILFTDSANNVYKQYEDMVVSCGCR 495

RESULT 12
US-09-813-398-37
; Sequence 37, Application US/09813398
; Patent No. US20020169292A1
; GENERAL INFORMATION:
; APPLICANT: Bruce D. Weintraub
; APPLICANT: Maribz W. Szklinski
; APPLICANT: University of Maryland
; TITLE OF INVENTION: CYSTINE KNOT GROWTH FACTOR MUTANTS
; FILE REFERENCE: IOFMD,003C1
; CURRENT APPLICATION NUMBER: US/09/813,398
; CURRENT FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: PCT/US99/05908
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: PCT/US98/19772
; PRIOR FILING DATE: 1998-09-22
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 37
; LENGTH: 502
; TYPE: PRT
; ORGANISM: HOMO SAPIEN
US-09-813-398-37

Query Match      98.5%; Score 639; DB 10; Length 502;
Best Local Similarity 98.3%; Pred. No. 4,1e-61;
Matches 117; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Cy 1 PLATROGKRPSSKLNKARCSRKALHVNFKDMGMDMTIAPLEYAFHCGGLCEPPLRSHTL 60
Db 384 PSATROGGRPSKLNKARCSRKALHVNFKDMGMDMTIAPLEYAFHCGGLCEPPLRSHTL 443
Cy 61 PTNNAVIGTLMNSMDPESTPTACVPTRLSPISILFTDSANNVYKQYEDMVVSCGCR 119
Db 444 PTNNAVIGTLMNSMDPESTPTCCVPTRLSPISILFTDSANNVYKQYEDMVVSCGCR 502

RESULT 13
US-09-730-772-13
; Sequence 13, Application US/09730772
; Patent No. US2001001131A1
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GENERAL INFORMATION:
APPLICANT: Luyten, Frank P.
APPLICANT: Moos, Jr., Malcolm
APPLICANT: Chang, Steven Chao-Huan
TITLE OF INVENTION: CARTILAGE-DERIVED MORPHOGENETIC
PROTEINS
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive, 16th Floor
CITY: Newport Beach
STATE: CA
COUNTRY: U.S.A.
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/730,772
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/836,081
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Bartfeld, Neil S
REGISTRATION NUMBER: 39,901
REFERENCE/DOCKET NUMBER: NIH099.001APC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-235-8550
TELEFAX: 619-235-0176
TELEX:
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 501 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-730-772-13

Query Match 96.9%; Score 629; DB 9; Length 501;
Best Local Similarity 97.5%; Pred. No. 5.1e-60;
Matches 116; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 PLATROGKRPBKVKARCSRKALHVNFKMGMDWIIAPLEYEAFHCEGCEPRLSHLE 60
DB 383 PSATROGKRPBKVKARCSRKALHVNFKMGMDWIIAPLEYEAFHCEGCEPRLSHLE 442
QY 61 PTNHAVIQTLNMSMDPESTPTTACVPTRLSPISILFTDSANNVVKQYEDMVVESCGR 119
DB 443 PTNHAVIQTLNMSMDPESTPTTCCVPTRLSPISILFTDSANNVVKQYEDMVVESCGR 501

RESULT 14
US-09-735-849-13
Sequence 13, Application US/09735849
Patent No. US20010037017A1
GENERAL INFORMATION:
APPLICANT: Luyten, Frank P.
APPLICANT: Moos, Jr., Malcolm
APPLICANT: Chang, Steven Chao-Huan
TITLE OF INVENTION: CARTILAGE-DERIVED MORPHOGENETIC
PROTEINS
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive, 16th Floor
CITY: Newport Beach
STATE: CA
COUNTRY: U.S.A.
```

```

ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/735,849
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/836,081
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Bartfeld, Neil S
REGISTRATION NUMBER: 39,901
REFERENCE/DOCKET NUMBER: NIH099.001APC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-235-8550
TELEFAX: 619-235-0176
TELEX:
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 501 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-735-849-13

Query Match 96.9%; Score 629; DB 9; Length 501;
Best Local Similarity 97.5%; Pred. No. 5.1e-60;
Matches 116; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 PLATROGKRPBKVKARCSRKALHVNFKMGMDWIIAPLEYEAFHCEGCEPRLSHLE 60
DB 383 PSATROGKRPBKVKARCSRKALHVNFKMGMDWIIAPLEYEAFHCEGCEPRLSHLE 442
QY 61 PTNHAVIQTLNMSMDPESTPTTACVPTRLSPISILFTDSANNVVKQYEDMVVESCGR 119
DB 443 PTNHAVIQTLNMSMDPESTPTTCCVPTRLSPISILFTDSANNVVKQYEDMVVESCGR 501

RESULT 15
US-10-379-830-13
Sequence 13, Application US/10379830
Publication No. US20030176683A1
GENERAL INFORMATION:
APPLICANT: Luyten, Frank P.
APPLICANT: Moos, Jr., Malcolm
APPLICANT: Chang, Steven Chao-Huan
TITLE OF INVENTION: CARTILAGE-DERIVED MORPHOGENETIC
PROTEINS
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive, 16th Floor
CITY: Newport Beach
STATE: CA
COUNTRY: U.S.A.
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/379,830
FILING DATE: 03-Mar-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/730,772
FILING DATE: 30-NOV-2000
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APPLICATION NUMBER: 08/836,081
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Bartfeld, Neil S
REGISTRATION NUMBER: 39,901
REFERENCE/DOCKET NUMBER: NI099.001APC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-235-8550
TELEFAX: 619-235-0176
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 501 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-10-379-830-13

Query Match 96.9%; Score 629; DB 12; Length 501;
Best Local Similarity 97.5%; Pred. No. 5.1e-60;
Matches 116; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 PLATROGRPSKNTKARCSKALHVNFKDMGMDNITAPLEYBAFHCGLCFPIRSHLE 60
DB 383 PSATROGRPSKNTKARCSKALHVNFKDMGMDNITAPLEYBAFHCGLCFPIRSHLE 442
QY 61 PTNHAVIDTLMNSMDPESTPTACVPTRTSPISITIFIDSANNVYKQYEDMWVESCGCR 119
DB 443 PTNHAVIDTLMNSMDPESTPTCCVPTRTSPISITIFIDSANNVYKQYEDMWVESCGCR 501

Search completed: February 18, 2004, 17:48:54
Job time : 34 secs

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OM protein - protein search, using sw model

Run on: February 18, 2004, 17:41:20 ; Search time 21 Seconds

(without alignments)
239.762 Million cell updates/sec

Title: US-09-701-121-2

Perfect score: 649
Sequence: 1 PLATROGKRPKNLAKRCSR.....ANNVYKQYEDMVESGCCR 119

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: Issued Patents, AA: *
2: /cgn2_6/ptodata/1/1aa/5A_COMB.pep: *
3: /cgn2_6/ptodata/1/1aa/5B_COMB.pep: *
4: /cgn2_6/ptodata/1/1aa/6A_COMB.pep: *
5: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep: *
6: /cgn2_6/ptodata/1/1aa/backfile1.pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|----------------------------------------|
| 1 | 645 | 99.4 | 120 | 1 | US-08-362-670B-4 Sequence 4, Appl |
| 2 | 645 | 99.4 | 120 | 3 | US-08-333-576C-4 Sequence 4, Appl |
| 3 | 645 | 99.4 | 120 | 5 | PCT-US94-14030A-4 Sequence 4, Appl |
| 4 | 645 | 99.4 | 120 | 5 | PCT-US94-14030A-4 Sequence 3, Appl |
| 5 | 645 | 99.4 | 401 | 3 | US-08-289-222E-3 Sequence 2, Appl |
| 6 | 645 | 99.4 | 401 | 3 | US-08-289-222E-3 Sequence 1, Appl |
| 7 | 645 | 99.4 | 501 | 2 | US-08-288-508C-2 Sequence 1, Appl |
| 8 | 645 | 99.4 | 501 | 4 | US-08-81-490B-1 Sequence 13, Appl |
| 9 | 640 | 98.6 | 119 | 1 | US-08-455-559-13 Sequence 13, Appl |
| 10 | 640 | 98.6 | 119 | 5 | PCT-US94-00657-13 Sequence 10, Appl |
| 11 | 640 | 98.6 | 119 | 5 | PCT-US94-00657-13 Sequence 10, Appl |
| 12 | 640 | 98.6 | 495 | 3 | US-09-145-060-10 Sequence 10, Appl |
| 13 | 640 | 98.6 | 495 | 3 | US-09-145-060-10 Sequence 10, Appl |
| 14 | 640 | 98.6 | 495 | 5 | PCT-US94-00657-10 Sequence 10, Appl |
| 15 | 559 | 86.1 | 102 | 1 | US-08-335-583C-51 Sequence 51, Appl |
| 16 | 559 | 86.1 | 102 | 2 | US-08-288-508C-13 Sequence 13, Appl |
| 17 | 559 | 86.1 | 102 | 3 | US-08-289-222E-22 Sequence 22, Appl |
| 18 | 559 | 86.1 | 102 | 3 | US-09-054-526E-22 Sequence 22, Appl |
| 19 | 543 | 83.7 | 119 | 1 | US-08-581-529E-7 Sequence 7, Appl |
| 20 | 543 | 83.7 | 119 | 3 | US-09-097-616-7 Sequence 7, Appl |
| 21 | 543 | 83.7 | 119 | 5 | PCT-US94-0776E-7 Sequence 7, Appl |
| 22 | 543 | 83.7 | 134 | 1 | US-08-581-529E-6 Sequence 6, Appl |
| 23 | 543 | 83.7 | 134 | 5 | US-09-097-616-6 Sequence 6, Appl |
| 24 | 543 | 83.7 | 134 | 5 | PCT-US94-0776E-6 Sequence 6, Appl |
| 25 | 540 | 83.2 | 321 | 1 | US-08-362-670B-26 Sequence 26, Appl |
| 26 | 540 | 83.2 | 321 | 1 | US-08-333-576C-26 Sequence 26, Appl |
| 27 | 540 | 83.2 | 321 | 3 | US-08-808-324-26 Sequence 26, Appl |

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|----|-----|------|-----|---|-----------------------------------------|
| 28 | 540 | 83.2 | 321 | 5 | PCT-US94-14030A-26 Sequence 26, Appl |
| 29 | 538 | 82.9 | 263 | 1 | US-08-362-670B-32 Sequence 32, Appl |
| 30 | 538 | 82.9 | 263 | 3 | US-08-333-576C-32 Sequence 32, Appl |
| 31 | 538 | 82.9 | 263 | 3 | US-08-808-324-32 Sequence 32, Appl |
| 32 | 538 | 82.9 | 263 | 5 | PCT-US94-14030A-32 Sequence 32, Appl |
| 33 | 494 | 76.1 | 129 | 1 | US-08-360-914B-15 Sequence 15, Appl |
| 34 | 494 | 76.1 | 129 | 1 | US-08-741-589A-13 Sequence 13, Appl |
| 35 | 494 | 76.1 | 294 | 1 | US-08-362-670B-2 Sequence 2, Appl |
| 36 | 494 | 76.1 | 294 | 3 | US-08-333-576C-2 Sequence 2, Appl |
| 37 | 494 | 76.1 | 294 | 3 | US-08-808-324-2 Sequence 2, Appl |
| 38 | 494 | 76.1 | 294 | 5 | PCT-US94-14030A-2 Sequence 2, Appl |
| 39 | 494 | 76.1 | 388 | 1 | US-08-362-670B-34 Sequence 34, Appl |
| 40 | 494 | 76.1 | 388 | 3 | US-08-333-576C-34 Sequence 34, Appl |
| 41 | 494 | 76.1 | 388 | 5 | US-08-808-324-34 Sequence 34, Appl |
| 42 | 494 | 76.1 | 388 | 5 | PCT-US94-14030A-34 Sequence 34, Appl |
| 43 | 494 | 76.1 | 411 | 1 | US-08-362-670B-28 Sequence 28, Appl |
| 44 | 494 | 76.1 | 411 | 3 | US-08-333-576C-28 Sequence 28, Appl |
| 45 | 494 | 76.1 | 411 | 3 | US-08-808-324-28 Sequence 28, Appl |

ALIGNMENTS

RESULT 1

US-08-362-670B-4
Sequence 4, Application US/08362670B
Patent No. 5658882

GENERAL INFORMATION:

APPLICANT: Celeste, Anthony J.
APPLICANT: Wozney, John
APPLICANT: Rosen, Vicki A.
APPLICANT: Wolfman, Neil
APPLICANT: Thomson, Gerald H.
APPLICANT: Melton, Douglas A.
TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSER: GENETICS INSTITUTE, INC.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: USA
ZIP: 02140

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/362,670B
FILING DATE: December 22, 1994
CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:
NAME: Lazat, Steven R.
REGISTRATION NUMBER: 32,618
REFERENCE/DOCKET NUMBER: 5202-D
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617 498-8260
TELEFAX: 617 876-5851

INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-362-670B-4

Query Match 99.4%; Score 645; DB 1; Length 120;
Best Local Similarity 99.2%; Pred. No. 1.4e-64;
Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLATROGKRPKNLAKRCSRKALHNFKMGMDMTIALTEAFHFCGLCFPLRSHLE 60

Db 2 PLATROGKRPBKNLAKRCRKALHVNFKMGWMDWITAPLEYAFHCEGLCEPFLRSHLE 61
QY 61 PTNNAVIQITLMSNDPESTPTACVPTRLSPISILFTDSANNVYKQYEDMVVESCGR 119
Db 62 PTNNAVIQITLMSNDPESTPTCCVPTRLSPISILFTDSANNVYKQYEDMVVESCGR 120

RESULT 2
US-08-333-576C-4
Sequence 4, Application US/08333576C
Patent No. 6027919
GENERAL INFORMATION:
APPLICANT: Celeste, Anthony J.
APPLICANT: Wozney, John
APPLICANT: Rosen, Vicki A.
APPLICANT: Wolman, Neil
APPLICANT: Thomsen, Gerald H.
APPLICANT: Melton, Douglas A.
TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENETICS INSTITUTE, INC.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: USA
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/333,576C
FILING DATE: No. 6027919ember 2, 1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Lazar, Steven R.
REGISTRATION NUMBER: 32,618
REFERENCE/DOCKET NUMBER: 5202-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617 498-8260
TELEFAX: 617 876-5851
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-333-576C-4

Query Match 99.4%; Score 645; DB 3; Length 120;
Best Local Similarity 99.2%; Pred. No. 1,4e-64;
Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 PLATROGKRPBKNLAKRCRKALHVNFKMGWMDWITAPLEYAFHCEGLCEPFLRSHLE 60
Db 2 PLATROGKRPBKNLAKRCRKALHVNFKMGWMDWITAPLEYAFHCEGLCEPFLRSHLE 61
QY 61 PTNNAVIQITLMSNDPESTPTACVPTRLSPISILFTDSANNVYKQYEDMVVESCGR 119
Db 62 PTNNAVIQITLMSNDPESTPTCCVPTRLSPISILFTDSANNVYKQYEDMVVESCGR 120

RESULT 3
US-08-808-324-4
Sequence 4, Application US/08808324
Patent No. 6284872
GENERAL INFORMATION:
APPLICANT: Celeste, Anthony J.
APPLICANT: Wozney, John
APPLICANT: Rosen, Vicki A.
APPLICANT: Wolman, Neil

APPLICANT: Thomsen, Gerald H.
APPLICANT: Melton, Douglas A.
TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENETICS INSTITUTE, INC.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: USA
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/808,324
FILING DATE: Herewith
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Lazar, Steven R.
REGISTRATION NUMBER: 32,618
REFERENCE/DOCKET NUMBER: 5202-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617 498-8260
TELEFAX: 617 876-5851
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-808-324-4

Query Match 99.4%; Score 645; DB 3; Length 120;
Best Local Similarity 99.2%; Pred. No. 1,4e-64;
Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLATROGKRPBKNLAKRCRKALHVNFKMGWMDWITAPLEYAFHCEGLCEPFLRSHLE 60
Db 2 PLATROGKRPBKNLAKRCRKALHVNFKMGWMDWITAPLEYAFHCEGLCEPFLRSHLE 61
QY 61 PTNNAVIQITLMSNDPESTPTACVPTRLSPISILFTDSANNVYKQYEDMVVESCGR 119
Db 62 PTNNAVIQITLMSNDPESTPTCCVPTRLSPISILFTDSANNVYKQYEDMVVESCGR 120

RESULT 4
PCT-US94-14030A-4
Sequence 4, Application PC/TUS9414030A
GENERAL INFORMATION:
APPLICANT: GENETICS INSTITUTE, INC.
APPLICANT: PRESIDENT AND FELLOWS OF HARVARD COLLEGE
TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENETICS INSTITUTE, INC.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: USA
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/14030A
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/164,103
FILING DATE: 07-DEC-1993
APPLICATION NUMBER: US 08/117,780
FILING DATE: 25-MAR-1994
APPLICATION NUMBER: US 08/333,576
FILING DATE: 02-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: LAZAR, STEVEN R.
REGISTRATION NUMBER: 32,618
REFERENCE/DOCKET NUMBER: 5202D-PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617 498-8260
TELEFAX: 617 876-5851
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US94-14030A-4

Query Match 99.4%; Score 645; DB 5; Length 120;
Best Local Similarity 99.2%; Pred. No. 1.4e-64;
Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLATROGRKPSKNTKARCSRKALHVNFKDMGMDWIIAPLEYEAHCGLCPEPRLRSHLE 60
DB 2 PLATROGRKPSKNTKARCSRKALHVNFKDMGMDWIIAPLEYEAHCGLCPEPRLRSHLE 61
QY 61 PTNAVAVIQTLMNSMDPESTPTTACVPTRLSPISILFIDSANNVVKQYEDMVVESCGR 119
DB 62 PTNAVAVIQTLMNSMDPESTPTTACVPTRLSPISILFIDSANNVVKQYEDMVVESCGR 120

RESULT 5

US-08-289-222E-3

Sequence 3, Application US/08289222E

Patent No. 6120760

GENERAL INFORMATION:

APPLICANT: HOTTEN, GERTRUD

APPLICANT: NEIDHARDT, HELGE

APPLICANT: BECHTOLD, ROLF

APPLICANT: POHL, JENS

TITLE OF INVENTION: GROWTH/DIFFERENTIATION FACTORS OF THE TGF-B

NUMBER OF SEQUENCES: 53

CORRESPONDENCE ADDRESS:

ADDRESSEE: NIKAIIDO, MARWELSTEIN, MURRAY & ORAM

STREET: 655 FIFTEENTH STREET, N. W., G STREET LOBBY,

STREET: SUITE 330

CITY: WASHINGTON

STATE: DC

COUNTRY: USA

ZIP: 20005-5701

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/289,222E

FILING DATE: 25-AUG-1999

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/289,222

FILING DATE: 12-AUG-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: DE P 44 23 190.3

FILING DATE: 07-JUL-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: EPO 92102324.8

FILING DATE: 12-FEB-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/EP93/00350
FILING DATE: 12-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: KITTS, MONICA CHIN
REGISTRATION NUMBER: 36,105
REFERENCE/DOCKET NUMBER: P564-9021
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/638-4810
TELEFAX: 202/638-5000
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 401 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-289-222E-3

Query Match 99.4%; Score 645; DB 3; Length 401;
Best Local Similarity 99.2%; Pred. No. 6.2e-64;
Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLATROGRKPSKNTKARCSRKALHVNFKDMGMDWIIAPLEYEAHCGLCPEPRLRSHLE 60
DB 283 PLATROGRKPSKNTKARCSRKALHVNFKDMGMDWIIAPLEYEAHCGLCPEPRLRSHLE 342
QY 61 PTNAVAVIQTLMNSMDPESTPTTACVPTRLSPISILFIDSANNVVKQYEDMVVESCGR 119
DB 343 PTNAVAVIQTLMNSMDPESTPTTACVPTRLSPISILFIDSANNVVKQYEDMVVESCGR 401

RESULT 6

US-09-054-526B-3

Sequence 3, Application US/09054526B

Patent No. 6197550

GENERAL INFORMATION:

APPLICANT: H TTEN, GERTRUD

APPLICANT: NEIDHARDT, HELGE

APPLICANT: BECHTOLD, ROLF

APPLICANT: POHL, JENS

TITLE OF INVENTION: DNA SEQUENCES ENCODING NOVEL

TITLE OF INVENTION: GROWTH/DIFFERENTIATION FACTORS

NUMBER OF SEQUENCES: 53

CORRESPONDENCE ADDRESS:

ADDRESSEE: NIKAIIDO, MARWELSTEIN, MURRAY & ORAM LLP

STREET: 655 FIFTEENTH STREET, N. W., G STREET LOBBY,

STREET: SUITE 330

CITY: WASHINGTON

STATE: DC

COUNTRY: USA

ZIP: 20005-5701

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/054,526B

FILING DATE: 03-APR-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/289,222

FILING DATE: 12-AUG-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: DE P 44 23 190.3

FILING DATE: 01-JUL-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: EPO 92102324.8

FILING DATE: 12-FEB-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/EP93/00350

FILING DATE: 12-FEB-1993

ATTORNEY/AGENT INFORMATION:

NAME: KITTS, MONICA CHIN

REGISTRATION NUMBER: 36,105
REFERENCE/DOCKET NUMBER: P564-8005
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/638-5000
TELEFAX: 202/638-4810
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 401 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-054-5268-3

Query Match 99.4%; Score 645; DB 3; Length 401;
Best Local Similarity 99.2%; Pred. No. 6.2e-64;
Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLATROGKRPSPKNIKARCSRKALHVNFKDGMDDMIAPLEYAFHCEGLCEPPLRSHTL 60
DB 283 PLATROGKRPSPKNIKARCSRKALHVNFKDGMDDMIAPLEYAFHCEGLCEPPLRSHTL 342

QY 61 PTNHAVIQTLNMSMDPESTPTCTACVPTRLSPISILFTIDSANNVYKQYEDMVVSCGCR 119
DB 343 PTNHAVIQTLNMSMDPESTPTCTACVPTRLSPISILFTIDSANNVYKQYEDMVVSCGCR 401

RESULT 7
US-08-288-508C-2
Sequence 2, Application US/08288508C
Patent No. 5994094
GENERAL INFORMATION:
APPLICANT: H tten, Gertrud
APPLICANT: Neidhardt, Helge
APPLICANT: Paulista, Michael
TITLE OF INVENTION: NEW GROWTH/DIFFERENTIATING FACTOR OF
TITLE OF INVENTION: THE TGF- FAMILY
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nikaido, Marmelstein, Murray & Oram LLP
STREET: 655 Fifteenth Street N.W. Suite 330
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-5701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/288,508C
FILING DATE: 10-AUG-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 43 26 829.3
FILING DATE: 10-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 44 18 222.8
FILING DATE: 25-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 44 20 157.5
FILING DATE: 09-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: JAHNS, Kristina M.
REGISTRATION NUMBER: P-41,092
REFERENCE/DOCKET NUMBER: P564-4019
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)638-5000
TELEFAX: (202)638-4810
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 501 amino acids

TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-288-508C-2

Query Match 99.4%; Score 645; DB 2; Length 501;
Best Local Similarity 99.2%; Pred. No. 8.3e-64;
Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLATROGKRPSPKNIKARCSRKALHVNFKDGMDDMIAPLEYAFHCEGLCEPPLRSHTL 60
DB 383 PLATROGKRPSPKNIKARCSRKALHVNFKDGMDDMIAPLEYAFHCEGLCEPPLRSHTL 442

QY 61 PTNHAVIQTLNMSMDPESTPTCTACVPTRLSPISILFTIDSANNVYKQYEDMVVSCGCR 119
DB 443 PTNHAVIQTLNMSMDPESTPTCTACVPTRLSPISILFTIDSANNVYKQYEDMVVSCGCR 501

RESULT 8
US-08-981-490B-1
Sequence 1, Application US/08981490B
Patent No. 6531450
GENERAL INFORMATION:
APPLICANT: Hotten, Gertrud
APPLICANT: Pohl, Jens
APPLICANT: Bechtold, Rolf
APPLICANT: Paulista, Michael
APPLICANT: Unsicker, Klaus
TITLE OF INVENTION: USE OF MP52 OR MP121 FOR TREATING AND PREVENTING DISEASES OF THE
TITLE OF INVENTION: NERVOUS SYSTEM
FILE REFERENCE: 100564-07032
CURRENT APPLICATION NUMBER: US/08/981,490B
CURRENT FILING DATE: 1998-05-18
PRIOR APPLICATION NUMBER: PCT/EP96/03065
PRIOR FILING DATE: 1996-07-12
PRIOR APPLICATION NUMBER: DE/195 25 416.3
PRIOR FILING DATE: 1995-07-12
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin version 3.1
SEQ ID NO 1
LENGTH: 501
TYPE: PRT
ORGANISM: Homo sapiens
US-08-981-490B-1

Query Match 99.4%; Score 645; DB 4; Length 501;
Best Local Similarity 99.2%; Pred. No. 8.3e-64;
Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLATROGKRPSPKNIKARCSRKALHVNFKDGMDDMIAPLEYAFHCEGLCEPPLRSHTL 60
DB 383 PLATROGKRPSPKNIKARCSRKALHVNFKDGMDDMIAPLEYAFHCEGLCEPPLRSHTL 442

QY 61 PTNHAVIQTLNMSMDPESTPTCTACVPTRLSPISILFTIDSANNVYKQYEDMVVSCGCR 119
DB 443 PTNHAVIQTLNMSMDPESTPTCTACVPTRLSPISILFTIDSANNVYKQYEDMVVSCGCR 501

RESULT 9
US-08-455-559-13
Sequence 13, Application US/08455559
Patent No. 5801014
GENERAL INFORMATION:
APPLICANT: LEE, SE-JIN
APPLICANT: HUYNH, THANH
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-5
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: SPENSLEY HORN JUBAS & LOBITZ
STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR
CITY: LOS ANGELES
STATE: CALIFORNIA
COUNTRY: US

ZIP: 90067
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,559
FILING DATE: 31-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/003,144
FILING DATE: 12-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: WETHERELL, JR. PH.D., JOHN R.
REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: PD2280
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/455-5100
TELEFAX: 619-455-5110
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
IMMEDIATE SOURCE:
CLONE: GDF-5
FEATURE:
NAME/KEY: Protein
LOCATION: 1.119
US-08-455-559-13

Query Match
Best Local Similarity 98.6%; Score 640; DB 1; Length 119;
Matches 117; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 PLATRGKRPSSKNLKARCSRKALHVNFKDGMWDWIIAPLEYAFHCEGLCEFPILRSHLE 60
DB 1 PLANQGRKRPSSKNLKARCSRKALHVNFKDGMWDWIIAPLEYAFHCEGLCEFPILRSHLE 60
QY 61 PTNHAVIQTLNMSMDPESTPPTACVPTRLSPISILFTDSANNVVKQYEDMVVESCGR 119
DB 61 PTNHAVIQTLNMSMDPESTPPTCCVPTRLSPISILFTDSANNVVKQYEDMVVESCGR 119

RESULT 10
US-09-145-060-13
Sequence 13, Application US/09145060
Patent No. 6245896
GENERAL INFORMATION:
APPLICANT: Lee, Se-Jin
APPLICANT: Huynh, Thanh
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-5
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: PasteQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/145,060
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/455,559

FILING DATE: 31-MAY-1995
APPLICATION NUMBER: 08/003,144
FILING DATE: 12-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Lisa A. Haile, Ph.D.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/057001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
IMMEDIATE SOURCE:
CLONE: GDF-5
US-09-145-060-13

Query Match
Best Local Similarity 98.6%; Score 640; DB 3; Length 119;
Matches 117; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 PLATRGKRPSSKNLKARCSRKALHVNFKDGMWDWIIAPLEYAFHCEGLCEFPILRSHLE 60
DB 1 PLANQGRKRPSSKNLKARCSRKALHVNFKDGMWDWIIAPLEYAFHCEGLCEFPILRSHLE 60
QY 61 PTNHAVIQTLNMSMDPESTPPTACVPTRLSPISILFTDSANNVVKQYEDMVVESCGR 119
DB 61 PTNHAVIQTLNMSMDPESTPPTCCVPTRLSPISILFTDSANNVVKQYEDMVVESCGR 119

RESULT 11
PCT-US94-00657-13
Sequence 13, Application PC/TUS9400657
GENERAL INFORMATION:
APPLICANT: SE-JIN LEE
APPLICANT: HUYNH, THANH
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-5
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: SPENSLLEY HORN UTBAS & LUBITZ
STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR
CITY: LOS ANGELES
STATE: CALIFORNIA
COUNTRY: US
ZIP: 90067
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/00657
FILING DATE: 1/12/94
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: WETHERELL, JR. PH.D., JOHN R.
REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: PD2280
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/455-5100
TELEFAX: 619-455-5110
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
IMMEDIATE SOURCE:
CLONE: GDF-5

FEATURE:
NAME/KEY: Protein
LOCATION: 1..119
PCT-US94-00657-13

Query Match 98.6%; Score 640; DB 5; Length 119;
Best Local Similarity 98.3%; Pred. No. 4,9e-64;
Matches 117; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 PLATOGKRPSSKNLKARCSRKALHVNFKMGMDWIIAPLEYEAFHCGEGCEPPLRSHTLE 60
DB 1 PLANOGRPSKNLKARCSRKALHVNFKMGMDWIIAPLEYEAFHCGEGCEPPLRSHTLE 60
QY 61 PTNHAVIQTLNMSMDPESTPTACVPTRLSPISILFIDSANVNVVKQYEDMWVESCGCR 119
DB 61 PTNHAVIQTLNMSMDPESTPTACVPTRLSPISILFIDSANVNVVKQYEDMWVESCGCR 119

RESULT 12
US-08-455-559-10
Sequence 10, Application US/08455559
Patent No. 5801014
GENERAL INFORMATION:
APPLICANT: LEE, SE-JIN
APPLICANT: HUYNH, THANH
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-5
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: SPENSLEY HORN JUBAS & LUBITZ
STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR
CITY: LOS ANGELES
STATE: CALIFORNIA
COUNTRY: US
ZIP: 90067
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release 1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,559
FILING DATE: 31-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/003,144
FILING DATE: 12-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: WETHERELL, JR. PH.D., JOHN R.
REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: PD2280
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/455-5100
TELEFAX: 619-455-5110
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 495 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-455-559-10

Query Match 98.6%; Score 640; DB 1; Length 495;
Best Local Similarity 98.3%; Pred. No. 2.9e-63;
Matches 117; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 PLATOGKRPSSKNLKARCSRKALHVNFKMGMDWIIAPLEYEAFHCGEGCEPPLRSHTLE 60
DB 377 PLANOGRPSKNLKARCSRKALHVNFKMGMDWIIAPLEYEAFHCGEGCEPPLRSHTLE 436
QY 61 PTNHAVIQTLNMSMDPESTPTACVPTRLSPISILFIDSANVNVVKQYEDMWVESCGCR 119
DB 437 PTNHAVIQTLNMSMDPESTPTACVPTRLSPISILFIDSANVNVVKQYEDMWVESCGCR 495

RESULT 13
US-09-145-060-10
Sequence 10, Application US/09145060
Patent No. 624596
GENERAL INFORMATION:
APPLICANT: Lee, Se-Jin
APPLICANT: Huynh, Thanh
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-5
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSRO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/145,060
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/455,559
FILING DATE: 31-MAY-1995
APPLICATION NUMBER: 08/003,144
FILING DATE: 12-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Lisa A. Haller, Ph.D.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/057001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 495 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-09-145-060-10

Query Match 98.6%; Score 640; DB 3; Length 495;
Best Local Similarity 98.3%; Pred. No. 2.9e-63;
Matches 117; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 PLATOGKRPSSKNLKARCSRKALHVNFKMGMDWIIAPLEYEAFHCGEGCEPPLRSHTLE 60
DB 377 PLANOGRPSKNLKARCSRKALHVNFKMGMDWIIAPLEYEAFHCGEGCEPPLRSHTLE 436
QY 61 PTNHAVIQTLNMSMDPESTPTACVPTRLSPISILFIDSANVNVVKQYEDMWVESCGCR 119
DB 437 PTNHAVIQTLNMSMDPESTPTACVPTRLSPISILFIDSANVNVVKQYEDMWVESCGCR 495

RESULT 14
PCT-US94-00657-10
Sequence 10, Application PC/TUS9400657
GENERAL INFORMATION:
APPLICANT: SE-JIN LEE
APPLICANT: HUYNH, THANH
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-5
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: SPENSLEY HORN JUBAS & LUBITZ
STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR
CITY: LOS ANGELES
STATE: CALIFORNIA
COUNTRY: US

QY 1 PLATOGKRPSSKNLKARCSRKALHVNFKMGMDWIIAPLEYEAFHCGEGCEPPLRSHTLE 60
DB 377 PLANOGRPSKNLKARCSRKALHVNFKMGMDWIIAPLEYEAFHCGEGCEPPLRSHTLE 436
QY 61 PTNHAVIQTLNMSMDPESTPTACVPTRLSPISILFIDSANVNVVKQYEDMWVESCGCR 119
DB 437 PTNHAVIQTLNMSMDPESTPTACVPTRLSPISILFIDSANVNVVKQYEDMWVESCGCR 495

ZIP: 90067
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/00657
FILING DATE: 1/12/94
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: WETHERILL, JR. PH.D., JOHN R.
REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: FD3256 CIP OF PD2280
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/455-5100
TELEFAX: 619-455-5110
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 495 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US94-00657-10

Query Match 98.6%; Score 640; DB 5; Length 495;
Best Local Similarity 98.3%; Pred. No. 2,9e-65;
Matches 117; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 PLATROCKRPSKNLKARCSRKALHVNFKDMGMDWMIAPLEVEAFHCEGLCEPPLRSHLE 60
DB 377 PLNRQCKRPSKNLKARCSRKALHVNFKDMGMDWMIAPLEVEAFHCEGLCEPPLRSHLE 436
QY 61 PTNHAVIQTLMNSMDPEPTPTACVPTPLSPISILFTDSANNVYKQYEDMVVESCGR 119
DB 437 PTNHAVIQTLMNSMDPEPTPTACVPTPLSPISILFTDSANNVYKQYEDMVVESCGR 495

RESULT 15

US-08-335-583C-51
Sequence 51, Application US/08335583C
Patent No. 5693779
GENERAL INFORMATION:
APPLICANT: Moos Jr., Malcolm
APPLICANT: Wang, Shouwan
TITLE OF INVENTION: PRODUCTION AND USE OF
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobe, Martens, Olson and Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: CA
COUNTRY: USA
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/335,583C
FILING DATE:
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: NIH104.001A
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TELEPHONE: 714-760-0404
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INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 102 amino acids
TYPE: amino acids
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: C-terminal
ORIGINAL SOURCE:
US-08-335-583C-51

Query Match 86.1%; Score 559; DB 1; Length 102;
Best Local Similarity 99.0%; Pred. No. 4.3e-55;
Matches 101; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 18 CSRKALHVNFKDMGMDWMIAPLEVEAFHCEGLCEPPLRSHLEPTNHAVIQTLMNSMDPE 77
DB 1 CSRKALHVNFKDMGMDWMIAPLEVEAFHCEGLCEPPLRSHLEPTNHAVIQTLMNSMDPE 60
QY 78 STPTACVPTPLSPISILFTDSANNVYKQYEDMVVESCGR 119
DB 61 STPTACVPTPLSPISILFTDSANNVYKQYEDMVVESCGR 102

Search completed: February 18, 2004, 17:44:26
Job time: 21 secs